(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
1 August 2002 (01.08.2002)

PCT

(10) International Publication Number
WO 02/059271 A2

(51) International Patent Classification[7]: C12N

(21) International Application Number: PCT/US02/02176

(22) International Filing Date: 25 January 2002 (25.01.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/263,757	25 January 2001 (25.01.2001)	US
60/286,090	25 April 2001 (25.04.2001)	US
60/292,517	23 May 2001 (23.05.2001)	US

(71) Applicant *(for all designated States except US)*: **GENE LOGIC, INC.** [US/US]; 708 Quince Orchard Road, Gaithersburg, MD 20878 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **ORR, Michael, S.** [US/US]; c/o GENE LOGIC, INC., 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). **NATION, Michele** [US/US]; c/o GENE LOGIC, INC., 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). **DIGGANS, James, C.** [US/US]; c/o GENE LOGIC, INC., 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). **ZENG, Wen** [CN/US]; c/o GENE LOGIC, INC., 708 Quince Orchard Road, Gaithersburg, MD 20878 (US).

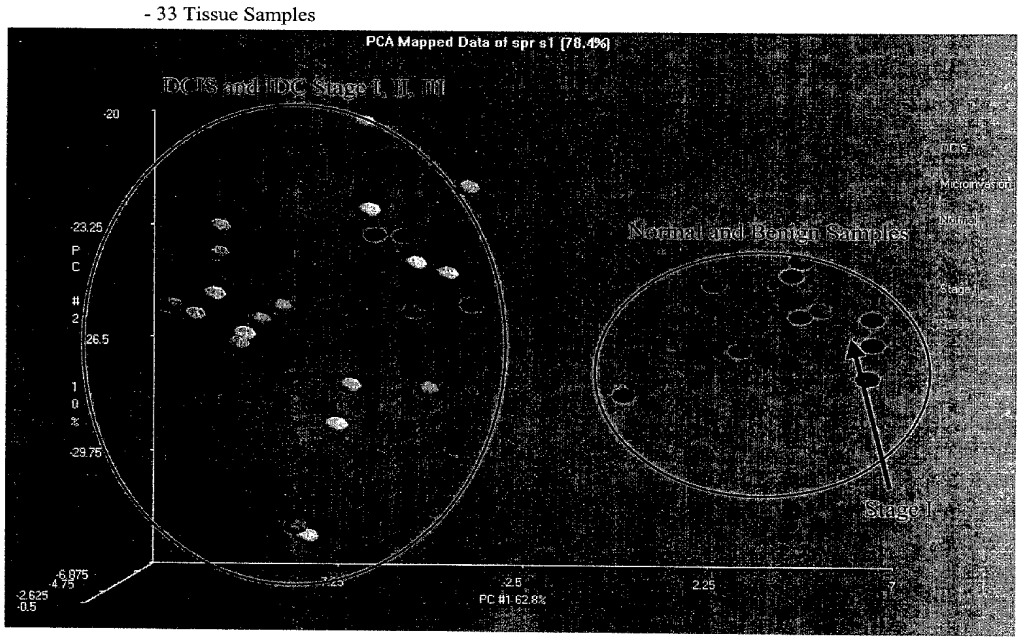
(74) Agent: **MORGAN, LEWIS & BOCKIUS LLP**; TUSCAN, Michael S., WEIMAR, Elizabeth C. et al., 1111 Pennsylvania Avenue, N.W., Washington, DC 20004 (US).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR,

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(54) Title: GENE EXPRESSION PROFILES IN BREAST TISSUE



(57) Abstract: The present invention results from the examination of tissue from breast carcinomas to identify genes differentially expressed between tumor biopsies and normal tissue. The invention includes diagnostic and screening methods using these genes as well as solid supports comprising oligonucleotide arrays that are complementary to or hybridize to the differentially expressed genes.

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GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

— *with sequence listing part of description published separately in electronic form and available upon request from the International Bureau*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

GENE EXPRESSION PROFILES IN BREAST TISSUE

INVENTORS: Michael S. Orr, Michele Nation, J.C. Diggans and Wen Zeng

RELATED APPLICATIONS

This application claims the priority of U.S. Provisional Application Nos. 60/263,757, filed January 25, 2001, 60/286,090, filed April 25, 2001, and 60/292,517, filed May 23, 2001, all of which are herein incorporated by reference in their entirety.

BACKGROUND OF THE INVENTION

One of the most pressing health issues today is breast cancer. In the industrial world, about one woman in every nine can expect to develop breast cancer in her lifetime. In the United States, it is the most common cancer amongst women, with an annual incidence of about 175,000 new cases and nearly 50,000 deaths. Despite an ongoing improvement in our understanding of the disease, breast cancer has remained resistant to medical intervention. Most clinical initiatives are focused on early diagnosis, followed by conventional forms of intervention, particularly surgery and chemotherapy. Such interventions are of limited success, particularly in patients where the tumor has undergone metastasis. There is a pressing need to improve the arsenal of therapies available to provide more precise and more effective treatment in a less invasive way. A promising area for the development of new modalities has emerged from recent understanding of the genetics of cancer.

One model used to characterize breast carcinogenesis asserts that normal cells undergo a multi-step process that broadly includes the steps of hyperplasia, pre-malignant change and *in situ* carcinoma. Multiple factors lead to atypical cell proliferation followed by carcinoma *in situ*. Carcinoma *in situ* is characterized as either ductal or lobular in form with the majority of invasive carcinomas being classified as ductal (85-95%). Among the ductal carcinomas, 15-20% encompass tubular, medullary, mucinous, papillary, adenoid, cystic, metaplastic, apocrine, squamous, secretory, lipid-rich, and cystic hypersecretory while the remaining ductal carcinomas are not specified.

To date, researchers have been able to identify a few genetic alterations believed to underlie tumor development. These genetic alterations include amplification of oncogenes and mutations that result in the loss of tumor suppressor genes. Tumor suppressor genes are genes that, in their wild-type alleles, express proteins that suppress abnormal cellular

proliferation. When the gene coding for a tumor suppressor protein is mutated or deleted, the resulting mutant protein or the complete lack of tumor suppressor protein expression may fail to correctly regulate cellular proliferation, and abnormal proliferation may take place, particularly if there is already existing damage to the cellular regulatory mechanism. A number of well-studied human tumors and tumor cell lines have missing or non-functional tumor suppressor genes. Examples of tumor suppressor genes include, but are not limited to, the retinoblastoma susceptibility gene or RB gene, the p53 gene, the deletion in colon carcinoma (DCC) gene and the neurofibromatosis type 1 (NF-1) tumor suppressor gene (Weinberg, *Science* 254,1138-1146 (1991)). Loss of function or inactivation of tumor suppressor genes may play a central role in the initiation and/or progression of a significant number of human cancers.

Classification of heterogeneous populations of tumor types is a daunting task; yet, studies utilizing gene expression patterns to identify subtypes of cancer have produced initial results (see Perou, C. M. *et al.*, *Proc Natl Acad Sci USA* 96, 9212-9217 (1999), Golub, T. R. *et al.*, *Science* 286, 531-7 (1999), Alizadeh, A. A. *et al.*, *Nature* 403, 503-11 (2000), Alon, U. *et al. Proc Natl Acad Sci U S A* 96, 6745-50 (1999) and Bittner, M. *et al.*, *Nature* 406, 536-40 (2000)). For example, molecular classification of B-cell lymphoma by gene expression profiling elucidated clinically distinct diffuse large-B-cell lymphoma subgroups (see Alizadeh *supra*). Stratification of patients based on their distinctive gene expression profiles may allow researchers to precisely group similar patient populations for evaluating chemotherapeutic agents. The more homogenous population of patients decreases the variability of patient-to-patient responses leading to the development of agents capable of eradicating specific subtypes of cancers previously unknown using standard classification techniques.

A study by Martin *et al.* (*Cancer Res* 60, 2232-8 (2000)) used a custom microarray composed of 124 genes discovered by differential display associated with either normal breast epithelial cells or from the MDA-MB-435 malignant breast tumor cell line. Using the custom microarray, researchers examined the relationship between expression patterns discovered by clustering a number of genes with clinical stages of breast cancer, indicating that gene expression patterns were capable of grouping breast tumors into distinct categories (Martin *et al.*, *supra*).

The utilization of gene expression profiles to classify tumors, to identify drug targets, to identify diagnostic markers and/or to gain further insights into the consequences of chemotherapeutic treatments could facilitate the design of more efficacious patient–

specific stratagems for treating a variety of cancers. In breast cancer, studies utilizing limited numbers of genes have classified tumors into subtypes based on gene expression profiles, and this study indicated a diversity of molecular phenotypes associated with breast tumors (Perou, C. M. *et al.*, *Nature* 406, 747-52 (2000).

Although these studies have demonstrated that expression profiling may be used to produce improvements in diagnosis of breast cancer as well as the development of improved therapeutic strategies, further studies are needed as only a small portion of the genome was studied and analyses containing greater numbers of genes will advance our understanding of breast tumors even further. Accordingly, there remains a need in the art for materials and methods that permit a more accurate diagnosis of breast cancer and, in particular, ductal carcinoma. In addition, there remains a need in the art for methods to treat and methods to identify agents that can effectively treat breast cancer. The present invention meets these and other needs.

SUMMARY OF THE INVENTION

The present invention is based on the discovery of the genes and their expression profiles associated with various types and stages of breast cancer.

The invention includes methods of diagnosing breast cancer in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from Tables 1-5; wherein differential expression of the genes in Tables 1-5 is indicative of breast cancer.

The invention also includes methods of detecting the progression of breast cancer. For instance, methods of the invention include detecting the progression of breast cancer in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from Tables 1-5; wherein differential expression of the genes in Tables 1-5 is indicative of breast cancer progression. In some preferred embodiments, PCA (Principal Component Analysis) based on all or a portion of the group of 50 genes identified in Table 1 may be used to differentiate between the different stages of breast cancer such as normal versus DCIS (ductal carcinoma *in-situ*) or DCIS versus microinvasive tissue samples. In some preferred embodiments, one or more genes may be selected from Tables 1, 3, 4 and/or 5.

In some aspects, the present invention provides a method of monitoring the treatment of a patient with breast cancer, comprising administering a pharmaceutical composition to the patient and preparing a gene expression profile from a cell or tissue

sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal breast cells or to a gene expression profile from a cell population comprising breast cancer cells or to both. In some preferred embodiments, the gene profile will include the expression level of one or more genes in Tables 1-5.

Another aspect of the present invention includes a method of treating a patient with breast cancer, comprising administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 1-5, preparing a gene expression profile from a cell or tissue sample from the patient comprising tumor cells and comparing the patient expression profile to a gene expression profile from an untreated cell population comprising breast cancer cells.

In another aspect, the present invention provides a method of identifying ductal carcinoma in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 1-5, wherein differential expression of the genes in Tables 1-5 is indicative of ductal carcinoma. In addition, by determining the expression level of two or more genes in the group of genes listed in Tables 1-5, one skilled in the art can differentiate between DCIS and a cribiform type of DCIS that is more prone to microinvasion.

In another aspect, the present invention provides a method of detecting the progression of carcinogenesis in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 1-5; wherein differential expression of the genes in Tables 1-5 is indicative of breast carcinogenesis. Figures 6 and 7 are a graphical representation of how the genes listed in Table 5 cluster with disease stages in breast cancer.

The invention further includes methods of screening for an agent capable of modulating the onset or progression of breast cancer, comprising the steps of exposing a cell to the agent; and detecting the expression level of two or more genes from Tables 1-5. In some embodiments, the breast cancer may be a ductal carcinoma. In some preferred embodiments, one or more genes may be selected from a group consisting of those listed in Tables 1, 3, 4 and/or 5. In some preferred methods, it may be desirable to detect all or nearly all of the genes in the tables.

The invention further includes compositions comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 1-5 as well as solid supports comprising at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to

a gene in Tables 1-5. In some preferred embodiments, one or more genes may be selected from a group consisting of those listed in Tables 1, 3, 4 and/or 5.

The invention further includes computer systems comprising a database containing information identifying the expression level in breast tissue of a set of genes comprising at least two genes in Tables 1-5 and a user interface to view the information. In some preferred embodiments, one or more genes may be selected from a group consisting of those listed in Tables 1, 3, 4 and/or 5. The database may further include sequence information for the genes, information identifying the expression level for the set of genes in normal breast tissue and cancerous tissue and may contain links to external databases such as GenBank.

Lastly, the invention includes methods of using the databases, such as methods of using the disclosed computer systems to present information identifying the expression level in a tissue or cell of at least one gene in Tables 1-5, comprising the step of comparing the expression level of at least one gene in Tables 1-5 in the tissue or cell to the level of expression of the gene in the database. In some preferred embodiments, two or more genes may be selected from a group consisting of those listed in Tables 1, 3, 4 and/or 5.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is an E- northern showing the expression of topoisomerase II alpha in various tissue types.

Figure 2 is an E-northern showing the expression of ICBP90 in various tissue types.

Figure 3 is an E-northern showing the expression of MCT4 gene.

Figure 4 is an E-northern showing the expression of the frizzled related protein.

Figure 5 is an E-northern showing the expression of an EST Affy ID AI668620.

Figure 6 is a PCA of the set of 28 samples using the top 50 genes identified by p-values.

Figure 7 is a PCA of the set of 33 samples using the top 50 genes and ESTs identified by p-values.

Figure 8 is a PCA of the set of 91 samples using the top 31 myo-lamina genes and ESTs.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

Many biological functions are accomplished by altering the expression of various genes through transcriptional (*e.g.*, through control of initiation, provision of RNA precursors, RNA processing, etc.) and/or translational control. For example, fundamental

biological processes such as cell cycle, cell differentiation and cell death, are often characterized by the variations in the expression levels of groups of genes.

Changes in gene expression also are associated with pathogenesis. For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over expression of oncogene/protooncogenes could lead to tumorgenesis or hyperplastic growth of cells (Marshall, *Cell* 64, 313-326 (1991); Weinberg, *Science*, 254, 1138-1146 (1991)). Thus, changes in the expression levels of particular genes (*e.g.*, oncogenes or tumor suppressors) serve as signposts for the presence and progression of various diseases.

Monitoring changes in gene expression may also provide certain advantages during drug screening and development. Often drugs are pre-screened for the ability to interact with a major target without regard to other effects the drugs have on cells. Often such other effects cause toxicity in the whole animal, which prevent the development and use of the potential drug.

Applicants have examined samples from normal breast tissue and from cancerous breast tissue to identify global changes in gene expression between tumor biopsies and normal tissue. These global changes in gene expression, also referred to as expression profiles, provide useful markers for diagnostic uses as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

The gene expression profiles described herein were derived from normal and tumor samples from female patients between the ages of 39 and 52 years old, and were from three different ethnic origins (Caucasian, African-American and Asian). Infiltrating Ductal Carcinoma (IDC) patient samples were studied for cancer-related expression, as 85% of the breast cancer patients were afflicted with this form of the disease.

Histological analysis of each tissue sample was performed and samples were segregated into either normal or malignant categories. The normal tissue samples were acquired from neighboring tissue of patients suffering from one of the following disorders: macromastia, mild fibrosis, infiltrating lobular carcinoma, or infiltrating ducal carcinoma, however; each tissue was diagnosed as normal by histological analysis. Samples were also characterized by the type and grade of IDC for each patient sample utilized in the study.

The present invention provides compositions and methods to detect the level of expression of genes that may be differentially expressed dependent upon the state of the cell, *i.e.*, normal versus cancerous. These expression profiles of genes provide molecular tools for evaluating toxicity, drug efficacy, drug metabolism, development, and disease

monitoring. Changes in the expression profile from a baseline profile can be used as an indication of such effects. Those skilled in the art can use any of a variety of known techniques to evaluate the expression of one or more of the genes and/or gene fragments identified in the instant application in order to observe changes in the expression profile in a tissue or sample of interest.

Definitions

In the description that follows, numerous terms and phrases known to those skilled in the art are used. In the interest of clarity and consistency of interpretation, the definitions of certain terms and phrases are provided.

As used herein, the phrase "detecting the level of expression" includes methods that quantify expression levels as well as methods that determine whether a gene of interest is expressed at all. Thus, an assay which provides a yes or no result without necessarily providing quantification of an amount of expression is an assay that requires "detecting the level of expression" as that phrase is used herein.

As used herein, oligonucleotide sequences that are complementary to one or more of the genes described herein, refers to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequence of said genes. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more nucleotide sequence identity to said genes.

"Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

The terms "background" or "background signal intensity" refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target nucleic acids and components of the oligonucleotide array (e.g., the oligonucleotide probes, control probes, the array substrate, etc.). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5%

to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation. Alternatively, background may be calculated as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (e.g., probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids). Background can also be calculated as the average signal intensity produced by regions of the array that lack any probes at all.

The phrase "hybridizing specifically to" refers to the binding, duplexing or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA.

Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100, preferably about 1000, more preferably about 10,000 and most preferably about 1,000,000 or more different nucleic acid hybridizations.

The terms "mismatch control" or "mismatch probe" refer to a probe whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence. For each mismatch (MM) control in a high-density array there typically exists a corresponding perfect match (PM) probe that is perfectly complementary to the same particular target sequence. The mismatch may comprise one or more bases that are not complementary to the corresponding bases of the target sequence.

While the mismatch(s) may be located anywhere in the mismatch probe, terminal mismatches are less desirable as a terminal mismatch is less likely to prevent hybridization of the target sequence. In a particularly preferred embodiment, the mismatch is located at or near the center of the probe such that the mismatch is most likely to destabilize the duplex with the target sequence under the test hybridization conditions.

The term "perfect match probe" refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a "test probe", a "normalization control" probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a "mismatch control" or "mismatch probe."

As used herein a "probe" is defined as a nucleic acid, preferably an oligonucleotide, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, U, C or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

The term "stringent conditions" refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH.

Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotide). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

The "percentage of sequence identity" or "sequence identity" is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may optionally comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical subunit (*e.g.*, nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

Homology or identity may be determined by BLAST (Basic Local Alignment Search Tool) analysis using the algorithm employed by the programs blastp, blastn, blastx,

tblastn and tblastx (Karlin *et al.*, *Proc Natl Acad Sci USA* 87, 2264-2268 (1990) and Altschul, *J Mol Evol* 36, 290-300 (1993), fully incorporated by reference) which are tailored for sequence similarity searching. The approach used by the BLAST program is to first consider similar segments between a query sequence and a database sequence, then to evaluate the statistical significance of all matches that are identified and finally to summarize only those matches which satisfy a preselected threshold of significance. For a discussion of basic issues in similarity searching of sequence databases, see Altschul *et al.*, (*Nature Genet* 6, 119-129 (1994)) which is fully incorporated by reference. The search parameters for histogram, descriptions, alignments, expect (*i.e.*, the statistical significance threshold for reporting matches against database sequences), cutoff, matrix and filter are at the default settings. The default scoring matrix used by blastp, blastx, tblastn, and tblastx is the BLOSUM62 matrix (Henikoff *et al.*, *Proc Natl Acad Sci USA* 89, 10915-10919, (1992) fully incorporated by reference). Four blastn parameters were adjusted as follows: Q=10 (gap creation penalty); R=10 (gap extension penalty); wink=1 (generates word hits at every winkth position along the query); and gapw=16 (sets the window width within which gapped alignments are generated). The equivalent Blastp parameter settings were Q=9; R=2; wink=1; and gapw=32. A Bestfit comparison between sequences, available in the GCG package version 10.0, uses DNA parameters GAP=50 (gap creation penalty) and LEN=3 (gap extension penalty) and the equivalent settings in protein comparisons are GAP=8 and LEN=2.

Uses of Differentially Expressed Genes

The present invention identifies those genes differentially expressed between normal breast tissue and cancerous breast tissue. One of skill in the art can select one or more of the genes identified as being differentially expressed in Tables 1-5 and use the information and methods provided herein to interrogate or test a particular sample. For a particular interrogation of two conditions or sources, it may be desirable to select those genes which display a great deal of difference in the expression pattern between the two conditions or sources. At least a two-fold difference may be desirable, but a three-fold, five-fold or ten-fold difference may be preferred in some instances. Interrogations of the genes or proteins can be performed to yield different information.

Diagnostic Uses for the Breast Cancer Markers

As described herein, the genes and gene expression information provided in Tables 1-5 may be used as diagnostic markers for the prediction or identification of the malignant state of breast tissue. For instance, a breast tissue sample or other sample from a patient may be assayed by any of the methods known to those skilled in the art, and the expression levels from one or more genes from Tables 1-5, may be compared to the expression levels found in normal breast tissue, tissue from breast carcinoma or both. Expression profiles generated from the tissue or other samples that substantially resemble an expression profile from normal or diseased breast tissue may be used, for instance, to aid in disease diagnosis. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described herein.

For example, genes over-expressed by 3-fold or greater, as well as having the smallest p-values from a t-test, were discovered by comparing 13 normal tissue samples and 15 infiltrating ductal carcinoma tissue samples composed of mostly stage II and III tissue samples. This analysis provided a set of genes (listed in Table 1) capable of distinguishing between the 13 normal and 15 tumor samples by PCA (Principal Component Analysis). In order to evaluate the ability of the genes to distinguish between normal and tumor tissue samples, a group of 33 tissues was selected from an existing gene expression database composed of normal, benign, DCIS (ductal carcinoma *in-situ*), microinvasive, stage I, stage II, and stage III breast cancer samples. PCA of the 33 tissue samples indicated that the genes selected based on the smallest p-values classified 32 out of 33 tissue samples correctly, while one stage I tissue sample was misclassified as a normal sample. Accordingly, these genes can be used diagnostically to differentiate normal/benign samples from tissue samples containing intraductal or infiltrating ductal carcinoma of the breast.

In another study, the PCA based on this group of genes indicates that these genes may be used to differentiate between the different stages of breast cancer such as normal versus DCIS or DCIS versus microinvasive tissue samples as graphically shown in Figures 6 and 7. The DCIS sample that contained focal microinvasions was grouped with the Stage I and II tumor samples. This group of genes may be used to determine if a DCIS sample contains microinvasions.

Use of the Breast Cancer Markers for Monitoring Disease Progression

Molecular expression markers for breast cancer can be used to confirm the type and progression of cancer made on the basis of morphological criteria. For example, normal

breast tissue could be distinguished from invasive carcinoma based on the level and type of genes expressed in a tissue sample. In some situations, identifications of cell type or source is ambiguous based on classical criteria. In these situations, the molecular expression markers of the present invention are useful.

In addition, progression of ductal carcinoma in situ to microinvasive carcinoma can be monitored by following the expression patterns of the involved genes using the molecular expression markers of the present invention. Monitoring of the efficacy of certain drug regimens can also be accomplished by following the expression patterns of the molecular expression markers.

In addition to the different disease progression stages which have been shown in Figures 6-7, as shown in the examples below, other developmental stages can be identified using these same molecular expression markers. While the importance of these markers in development has been shown here, variations in their expression may occur at other times. For example, variation in the expression level of one or more of the marker genes identified herein may be use to distinguish benign stages of breast cancer from malignant states.

As described above, the genes and gene expression information provided in Tables 1-5 may also be used as markers for the direct monitoring of disease progression, for instance, the development of breast cancer. For instance, a breast tissue sample or other sample from a patient may be assayed by any of the methods known to those of skill in the art, and the expression levels in the sample from a gene or genes from Tables 1-5 may be compared to the expression levels found in normal breast tissue, tissue from breast cancer or both. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described herein.

For instance, methods of this invention may use the 35 gene group (profile) composed of genes expressed in myoepithelial cells and basal lamina components in Table 3. The absence of both myoepithelial cells or basement membrane components usually indicates that the intraductal carcinoma is invasive. This group of 35 genes listed in Table 3 may be used to determine if myoepithelial and/or basal lamina components are present in a tissue sample. It includes 23 genes exhibiting a fold change of 3 fold or higher and 12 genes displaying a change of less than 3 fold. This group of 23 genes was used to distinguish between normal and tumor samples for a group of 33 tissue samples. In this study, the 23 genes were able to classify 32 out of 33 samples correctly and 26 out of 28 samples used to isolate this subgroup of genes. This group of genes can be used to identify

the various stages of ductal carcinoma tissues more discretely than the 50-gene set. The study also demonstrates that this group of genes can differentiate between DCIS and a cribiform type of DCIS that is more prone to microinvasion. Clinically, the ability to discern DCIS with microinvasions or phenotypes prone to microinvasions such as the cribiform type would allow subgrouping of the samples containing microinvasions as a type of patient that should be treated more aggressively than DCIS patients lacking this gene expression fingerprint. A subclass of DCIS (cribiform type) based on the gene expression fingerprint may be subgrouped as a micro invasive sample based on the gene expression pattern associated with this sample.

Use of the Breast Cancer Markers for Drug Screening

According to the present invention, potential drugs can be screened to determine if application of the drug alters the expression of one or more of the genes identified herein. This may be useful, for example, in determining whether a particular drug is effective in treating a particular patient with breast cancer. In the case where a gene's expression is affected by the potential drug such that its level of expression returns to normal, the drug is indicated in the treatment of breast cancer. Similarly, a drug which causes expression of a gene which is not normally expressed by epithelial cells in the breast, may be contra-indicated in the treatment of breast cancer.

According to the present invention, the genes identified in Tables 1-5 may also be used as markers to evaluate the effects of a candidate drug or agent on a cell, particularly a cell undergoing malignant transformation, for instance, a breast cancer cell or tissue sample. A candidate drug or agent can be screened for the ability to stimulate the transcription or expression of a given marker or markers (drug targets) or to down-regulate or inhibit the transcription or expression of a marker or markers. According to the present invention, one can also compare the specificity of a drug's effects by looking at the number of markers affected by the drug and comparing them to the number of markers affected by a different drug. A more specific drug will affect fewer transcriptional targets. Similar sets of markers identified for two drugs indicates a similarity of effects.

Assays to monitor the expression of a marker or markers as defined in Tables 1-5 may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agents action. Agents can be selected or designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

The agents of the present invention can be, as examples, peptides, small chemical molecules, vitamin derivatives, as well as carbohydrates, lipids, oligonucleotides and covalent and non-covalent combinations thereof. Dominant negative proteins, DNA encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" as used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see Grant in Molecular Biology and Biotechnology, Meyers, ed., VCH Publishers (1995)). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

Assay Formats

The genes identified as being differentially expressed in breast cancer may be used in a variety of nucleic acid detection assays to detect or quantify the expression level of a gene or multiple genes in a given sample. For example, traditional Northern blotting, nuclease protection, RT-PCR and differential display methods may be used for detecting gene expression levels.

The protein products of the genes identified herein can also be assayed to determine the amount of expression. Methods for assaying for a protein include Western blot, immunoprecipitation, radioimmunoassay. It is preferred, however, that the mRNA be assayed as an indication of expression. Methods for assaying for mRNA include Northern

blots, slot blots, dot blots, and hybridization to an ordered array of oligonucleotides. Any method for specifically and quantitatively measuring a specific protein or mRNA or DNA product can be used. However, methods and assays of the invention are most efficiently designed with PCR or array or chip hybridization-based methods for detecting the expression of a large number of genes.

Any hybridization assay format may be used, including solution-based and solid support-based assay formats. A preferred solid support is a high density array also known as a DNA chip or a gene chip. One variation of the DNA chip contains hundreds of thousands of discrete microscopic channels that pass completely through it. Probe molecules are attached to the inner surface of these channels, and molecules from the samples to be tested flow through the channels, coming into close proximity with the probes for hybridization. In one assay format, gene chips containing probes to at least two genes from Tables 1-5 may be used to directly monitor or detect changes in gene expression in the treated or exposed cell as described herein. Assays of the invention may measure the expression levels of about one, two, three, five, seven, ten, 15, 20, 25, 50, 100 or more genes in the Tables.

The genes and ESTs of the present invention may be assayed in any convenient sample form. For example, samples may be assayed in the form mRNA or reverse transcribed mRNA. Samples may be cloned or not and the samples or individual genes may be amplified or not. The cloning itself does not appear to bias the representation of genes within a population. However, it may be preferable to use polyA+ RNA as a source, as it can be used with less processing steps. In some embodiments, it may be preferable to assay the protein or peptide expressed by the gene.

The sequences of the expression marker genes of Tables 1-5 are available in the public databases. Tables 1-5 provide the Accession numbers and name for each of the sequences. The sequences of the genes in GenBank are herein expressly incorporated by reference in their entirety as of the filing date of this application. (see www.ncbi.nim.nih.gov).

Additional assay formats may be used to monitor the ability of the agent to modulate the expression of a gene identified in Tables 1-5. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to an agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.*, Molecular Cloning - A Laboratory Manual, Cold Spring Harbor

Laboratory Press, Cold Spring Harbor, NY (1989)). In some embodiments, it may be desirable to amplify one or more of the RNA molecules isolated prior to application of the RNA to the gene chip. Using techniques well known in the art, the RNA may be reverse transcribed and amplified in the form of DNA or may be reverse transcribed into DNA and the DNA used as a template for transcription to generate recombinant RNA. Any method that results in the production of a sufficient quantity of nucleic acid to be hybridized effectively to the gene chip may be used.

In another format, cell lines that contain reporter gene fusions between the open reading frame and or the 3' or 5' regulatory regions of a gene in Tables 1-5 and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.*, *Anal Biochem* 188, 245-254 (1990)). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of the nucleic acid.

In another assay format, cells or cell lines are first identified which express one or more of the gene products of the invention physiologically. Cells and/or cell lines so identified would preferably comprise the necessary cellular machinery to ensure that the transcriptional and/or translational apparatus of the cells would faithfully mimic the response of normal or cancerous breast tissue to an exogenous agent. Such machinery would likely include appropriate surface transduction mechanisms and/or cytosolic factors. Such cell lines may be, but are not required to be, derived from breast tissue. The cells and/or cell lines may then be contacted with an agent and the expression of one or more of the genes of interest may then be assayed. The genes may be assayed at the mRNA level and/or at the protein level.

In some embodiments, such cells or cell lines may be transduced or transfected with an expression vehicle (e.g., a plasmid or viral vector) containing an expression construct comprising an operable 5'-promoter containing end of a gene of interest identified in Tables 1-5 fused to one or more nucleic acid sequences encoding one or more antigenic fragments. The construct may comprise all or a portion of the coding sequence of the gene of interest which may be positioned 5'- or 3'- to a sequence encoding an antigenic fragment. The coding sequence of the gene of interest may be translated or un-translated after transcription of the gene fusion. At least one antigenic fragment may be translated. The antigenic

fragments are selected so that the fragments are under the transcriptional control of the promoter of the gene of interest and are expressed in a fashion substantially similar to the expression pattern of the gene of interest. The antigenic fragments may be expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides. In some embodiments, gene products of the invention may further comprise an immunologically distinct tag. Such a process is well known in the art (see Sambrook *et al., supra*).

Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells will be disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (e.g., ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the "agent-contacted" sample will be compared with a control sample where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the "agent-contacted" sample compared to the control will be used to distinguish the effectiveness of the agent.

Another embodiment of the present invention provides methods for identifying agents that modulate the levels, concentration or at least one activity of a protein(s) encoded by the genes in Tables 1-5. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

In one format, the relative amounts of a protein of the invention produced in a cell population that has been exposed to the agent to be tested may be compared to the amount produced in an un-exposed control cell population. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

Probe Design

Probes based on the sequences of the genes described herein may be prepared by any commonly available method. Oligonucleotide probes for assaying the tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases longer probes of at least 30, 40, or 50 nucleotides will be desirable.

One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The high density array will typically include a number of probes that specifically hybridize to the sequences of interest. See WO 99/32660 for methods of producing probes for a given gene or genes. In addition, in a preferred embodiment, the array will include one or more control probes.

High density array chips of the invention include "test probes." Test probes may be oligonucleotides that range from about 5 to about 500 or about 5 to about 50 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 40 nucleotides in length. In other particularly preferred embodiments, the probes are about 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences. DNA sequences may be isolated or cloned from natural sources or amplified from natural sources using natural nucleic acid as templates. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect.

In addition to test probes that bind the target nucleic acid(s) of interest, the high density array can contain a number of control probes. The control probes fall into three categories referred to herein as (1) normalization controls; (2) expression level controls; and (3) mismatch controls.

Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (*e.g.*, fluorescence

intensity) read from all other probes in the array are divided by the signal (*e.g.*, fluorescence intensity) from the control probes thereby normalizing the measurements.

Virtually any probe may serve as a normalization control. However, it is recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control(s) can also be selected to reflect the (average) base composition of the other probes in the array, however in a preferred embodiment, only one or a few probes are used and they are selected such that they hybridize well (i.e., no secondary structure) and do not match any target-specific probes.

Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typical expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to the β-actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

Mismatch controls may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (*e.g.*, stringent conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent). Preferred mismatch probes contain a central mismatch. Thus, for example, where a probe is a twenty-mer, a corresponding mismatch probe may have the identical sequence except for a single base mismatch (e.g., substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is directed. Mismatch probes also indicate whether a hybridization is specific or not. For example, if the target is present the perfect match probes should be consistently brighter

than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation. The difference in intensity between the perfect match and the mismatch probe (I(PM) - I(MM)) provides a good measure of the concentration of the hybridized material.

Nucleic Acid Samples

As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or process. Methods of isolating total mRNA are also well known to those of skill in the art. For example, methods of isolation and purification of nucleic acids are described in detail in Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology, Vol. 24, Hybridization With Nucleic Acid Probes: Theory and Nucleic Acid Probes, P. Tijssen, ed., Elsevier Press, New York (1993). Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and an RNA transcribed from the amplified DNA. One of skill in the art would appreciate that it may be desirable to inhibit or destroy RNase present in homogenates before homogenates can be used.

Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised *in vitro*, such as cell lines and tissue culture cells. Frequently the sample will be a "clinical sample" which is a sample derived from a patient. Typical clinical samples include, but are not limited to, breast tissue biopsy, sputum, blood, blood-cells (*e.g.*, white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom.

Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

Solid Supports

Solid supports containing oligonucleotide probes for differentially expressed genes can be any solid or semisolid support material known to those skilled in the art. Suitable examples include, but are not limited to, membranes, filters, tissue culture dishes, polyvinyl chloride dishes, beads, test strips, silicon or glass based chips and the like. Suitable glass wafers and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755). Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used. In some

embodiments, it may be desirable to attach some oligonucleotides covalently and others non-covalently to the same solid support.

A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, from 2, 10, 100, 1000 to 10,000, 100,000 or 400,000 of such features on a single solid support. The solid support, or the area within which the probes are attached may be on the order of a square centimeter.

Oligonucleotide probe arrays for expression monitoring can be made and used according to any techniques known in the art (see for example, Lockhart *et al.*, *Nat Biotechnol* 14, 1675-1680 (1996); McGall *et al.*, *Proc Nat Acad Sci USA* 93, 13555-13460 (1996)). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described herein. Such arrays my also contain oligonucleotides that are complementary or hybridize to at least 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 50, 70 or more the genes described herein.

Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a solid substrate by a variety of methods, including, but not limited to, light-directed chemical coupling, and mechanically directed coupling (see Pirrung *et al.*, (1992) U.S. Patent No. 5,143, 854; Fodor *et al.*, (1998) U.S. Patent No. 5,800,992; Chee *et al.*, (1998) U.S. Patent No. 5,837,832).

In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is derivatized with a silane reagent containing a functional group, *e.g.*, a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithogaphic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide

analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in Fodor *et al.*, WO 93/09668. High density nucleic acid arrays can also be fabricated by depositing pre-made or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

Hybridization

Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing (see Lockhart *et al.*, WO 99/32660). The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (*e.g.*, low temperature and/or high salt) hybrid duplexes (*e.g.*, DNA-DNA, RNA-RNA or RNA-DNA) will form even where the annealed sequences are not perfectly complementary. Thus, specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (*e.g.*, higher temperature or lower salt) successful hybridization requires fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency. In a preferred embodiment, hybridization is performed at low stringency, in this case in 6× SSPE-T at 37°C (0.005% Triton x-100) to ensure hybridization and then subsequent washes are performed at higher stringency (*e.g.*, 1× SSPE-T at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (*e.g.*, down to as low as 0.25× SSPET at 37°C to 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (*e.g.*, expression level control, normalization control, mismatch controls, *etc.*).

In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

Signal Detection

The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art (see Lockhart *et al.*, WO 99/32660).

Databases

The present invention includes relational databases containing sequence information, for instance for one or more of the genes of Tables 1-5, as well as gene expression information in various breast tissue samples. Databases may also contain information associated with a given sequence or tissue sample such as descriptive information about the gene associated with the sequence information, descriptive information concerning the clinical status of the tissue sample, or information concerning the patient from which the sample was derived. The database may be designed to include different parts, for instance a sequence database and a gene expression database. Methods for the configuration and construction of such databases are widely available, for instance, see Akerblom *et al.*, (1999) U.S. Patent No. 5,953,727, which is specifically incorporated herein by reference in its entirety.

The databases of the invention may be linked to an outside or external database. In a preferred embodiment, as described in Tables 1-5, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI).

Any appropriate computer platform may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such has those

available from Silicon Graphics. Client-server environments, database servers and networks are also widely available and appropriate platforms for the databases of the invention.

The databases of the invention may be used to produce, among other things, electronic Northern blots (E-Northerns) to allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell. The E-northern analysis can be used as a tool to discover tissue specific candidate therapeutic targets that are not over-expressed in tissues such as the liver, kidney, or heart. These tissue types often lead to detrimental side effects once drugs are developed and a first-pass screen to eliminate these targets early in the target discovery and validation process would be beneficial.

The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising at least one gene in Tables 1-5 comprising the step of comparing the expression level of at least one gene in Tables 1-5 in the tissue to the level of expression of the gene in the database. Such methods may be used to predict the physiological state of a given tissue by comparing the level of expression of a gene or genes in Tables 1-5 from a sample to the expression levels found in tissue from normal breast tissue, tissue from breast carcinoma or both. Such methods may also be used in the drug or agent screening assays as described herein.

Kits

The invention further includes kits combining, in different combinations, high-density oligonucleotide arrays, reagents for use with the arrays, signal detection and array-processing instruments, gene expression databases and analysis and database management software described above. The kits may be used, for example, to monitor the progression of breast cancer, to identify genes that show promise as new drug targets and to screen known and newly designed drugs as discussed above.

The databases packaged with the kits are a typically a compilation of expression patterns from human breast cancer tissue or cell lines and for gene and gene fragments as described herein (corresponding to the genes of Tables 1-5). In particular, the database software and packaged information include the expression results of Tables 1-5 that can be used to predict the cancerous state of a tissue sample by comparing the expression levels of the genes in the tissue or cell sample to the expression levels presented in Tables 1-5.

The kits may used in the pharmaceutical industry, where the need for early drug testing is strong due to the high costs associated with drug development, but where bioinformatics, in particular gene expression informatics, is still lacking. These kits will reduce the costs, time and risks associated with traditional new drug screening using cell cultures and laboratory animals. The results of large-scale drug screening of pre-grouped patient populations, pharmacogenomics testing, can also be applied to select drugs with greater efficacy and fewer side-effects. The kits may also be used by smaller biotechnology companies and research institutes who do not have the facilities for performing such large-scale testing themselves.

Databases and software designed for use with use with microarrays is discussed in Balaban *et al.*, (2001) U.S. Patent Nos. 6,229,911, a computer-implemented method for managing information, stored as indexed tables, collected from small or large numbers of microarrays, and 6,185,561 , a computer-based method with data mining capability for collecting gene expression level data, adding additional attributes and reformatting the data to produce answers to various queries. Chee *et al.*, (1999) U.S. Patent No. 5,974,164, disclose a software-based method for identifying mutations in a nucleic acid sequence based on differences in probe fluorescence intensities between wild type and mutant sequences that hybridize to reference sequences. The object of the method is to predict regions or positions of mutation.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The preceding working examples therefore, are illustrative only and should not be construed as limiting in any way the scope of the invention.

Examples

Example 1: Preparation of Breast Cancer Profiles

Tissue Sample Acquisition and Preparation

The patient tissue samples were derived from female patients; the average age for the normal and tumor samples was 39 and 52 years respectively. They stem from three different ethnic origins (Caucasian, African-American, and Asian). Furthermore, all tissue samples from Infiltrating Ductal Carcinoa (IDC) patient samples were studied for cancer-related expression, as 85% of the breast cancer patients were afflicted with this form of the

disease. The samples are composed of normal, benign, DCIS (ductal carcinoma *in-situ*), microinvasive, stage I, stage II, and stage III breast cancer samples.

Histological analysis of each of the tissue samples was performed and samples were segregated into either normal or malignant categories. The normal tissue samples were acquired from neighboring tissue of patients suffering from one of the following disorders: macromastia, mild fibrosis, infiltrating lobular carcinoma, or infiltrating ducal carcinoma, however; each tissue was diagnosed as normal by histological analysis.

With minor modifications, the sample preparation protocol followed the Affymetrix GeneChip Expression Analysis Manual. Frozen tissue was first ground to powder using the Spex Certiprep 6800 Freezer Mill. Total RNA was then extracted using Trizol (Life Technologies). The total RNA yield for each sample (average tissue weight of 300 mg) was 200-500 μg. Next, mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen). Since the mRNA was eluted in a final volume of 400 μl, an ethanol precipitation step was required to bring the concentration to 1 μg/μl. Using 1-5 μg of mRNA, double stranded cDNA was created using the SuperScript Choice system (Gibco-BRL). First strand cDNA synthesis was primed with a T7-(dT_{24}) oligonucleotide. The cDNA was then phenol-chloroform extracted and ethanol precipitated to a final concentration of 1 μg/μl.

From 2 μg of cDNA, cRNA was synthesized according to standard procedures. To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. After a 37°C incubation for six hours, the labeled cRNA was cleaned up according to the Rneasy Mini kit protocol (Qiagen). The cRNA was then fragmented (5× fragmentation buffer: 200 mM Tris-Acetate (pH 8.1), 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C.

55 μg of fragmented cRNA was hybridized on the human and the Human Genome U95 set of arrays for twenty-four hours at 60 rpm in a 45°C hybridization oven. The chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step in between. Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Following hybridization and scanning, the microarray images were analyzed for quality control, looking for major chip defects or abnormalities in hybridization signal. After all chips passed QC, the data was analyzed using Affymetrix GeneChip software (v3.0), and Experimental Data Mining Tool (EDMT) software (v1.0).

Gene Expression Analysis

All samples were prepared as described and hybridized onto the Affymetrix Human Genome U95 array. Each chip contains 16-20 oligonucleotide probe pairs per gene or cDNA clone. These probe pairs include perfectly matched sets and mismatched sets, both of which are necessary for the calculation of the average difference. The average difference is a measure of the intensity difference for each probe pair, calculated by subtracting the intensity of the mismatch from the intensity of the perfect match. This takes into consideration variability in hybridization among probe pairs and other hybridization artifacts that could affect the fluorescence intensities. Using the average difference value that has been calculated, an absolute call for each gene or EST is made.

The absolute call of present, absent or marginal is used to generate a Gene Signature, a tool used to identify those genes that are commonly present or commonly absent in a given sample set, according to the absolute call. For each set of samples, a median average difference was calculated using the average differences of each individual sample within the set. The median average difference typically must be greater than 20 to assure that the expression level is at least two standard deviations above the background noise of the hybridization. For the purposes of this study, only the genes and gene fragments with a median average difference greater than 20 were further studied in detail.

The Gene Signature for one set of samples is compared to the Gene Signature of another set of samples to determine the Gene Signature Differential. This comparison identifies the genes that are consistently present in one set of samples and consistently absent in the second set of samples.

The Gene Signature Curve is a graphic view of the number of genes consistently present in a given set of samples as the sample size increases, taking into account the genes commonly expressed among a particular set of samples, and discounting those genes whose expression is variable among those samples. The curve is also indicative of the number of samples necessary to generate an accurate Gene Signature. As the sample number increases, the number of genes common to the sample set decreases. The curve is generated using the positive Gene Signatures of the samples in question, determined by adding one sample at a time to the Gene Signature, beginning with the sample with the smallest number of present genes and adding samples in ascending order. The curve displays the sample size required for the most consistency and the least amount of expression variability from sample to sample. The point where this curve begins to level off represents the minimum

number of samples required for the Gene Signature. Graphed on the x-axis is the number of samples in the set, and on the y-axis is the number of genes in the positive Gene Signature. As a general rule, the acceptable percent of variability in the number of positive genes between two sample sets should be less than 5%.

Fold Change analysis

The data was first filtered to exclude all genes that showed no expression in any of the samples. The ratio (tumor/normal) was calculated by comparing the mean expression value for each gene in the breast cancer sample set against the mean expression value of that gene in the normal breast sample set. For Table 2, genes were included in the analysis if they had a fold change ≥ 3 in either direction, and a p-value < 0.05 as determined by a two-tail unequal variance t-test. Out of the ~60,000 genes surveyed by the Human Genome U95 set, 802 genes were present in the overall fold change analysis

Expression Profiles of Genes Differentially Expressed in Breast Cancer

Using the above described methods, genes that were predominantly over-expressed in breast cancer, or predominantly under-expressed in breast cancer were identified. Genes with consistent differential expression patterns provide potential targets for broad range diagnostics and therapeutics. For simplicity, applicants examined known genes by hierarchical cluster analysis developed by Eisen and colleagues to determine if functionally related genes would cluster together (see Eisen, *et al. Proc Natl Acad Sci USA* 95, 14863-14868 (1998)).

Table 2 lists the genes determined to be differentially expressed in cancerous breast tissues compared to normal breast tissue, with the fold change value for each gene. These genes or subsets of these genes comprise an overall breast cancer gene expression profile.

The well-characterized proliferation marker for breast cancer KI-67 had an average-fold change value of 2.8, which was calculated from 15 IDC tissue samples analyzed (see Gerdes, *Semin Cancer Biol* 1, 199-206 (1990)). As the fold change was below the present 3 fold criteria, the fold change value was not presented in Table 2. Some genes previously shown to be over or under expressed in breast cancer as indicated from the literature such as cytokeratins 5, 14, 15, 17, maspin, MMP 9 and 11, fibronectin, and pituitary tumor transforming 1, etc. are displayed in Table 2 as well as some genes such as p57(kip2), p63/p51/KET, mitosin, and pCDC55 whose expression levels were not previously known to vary in breast cancer.

The pituitary-tumor transforming 1 gene has been shown to produce *in vitro* and *in vivo* tumor-inducing activity (see Zhang *et al. Mol Endocrinol* 13, 156-66 (1999). In a recent publication, pituitary-tumor transforming 1 has been shown to be over-expressed in mammary adenocarcinomas (see Saez *et al. Oncogene* 18, 5473-6 (1999)). Also, another study discovered that all 48 colon carcinomas examined over-expressed PTTG1 as compared to normal colorectal tissue, and invasion of the surrounding tissue was associated with higher PTTG1 expression levels (see Heaney *et al.* Expression of pituitary-tumour transforming gene in colorectal tumours [see comments] *Lancet* 355, 716-9 (2000)).

Genes listed in Table 2, not reported in the literature to be over-expressed in human breast cancer tissues, include RAD2, FLS353, CKS2, cyclin-selective ubiquitin carrier protein E2-C, ZWINT, Lamin B1 and H2A.X. Although FLS353 has been recently found to be over-expressed in colorectal cancer (see Hufton *et al. FEBS Lett* 463, 77-82 (1999)), differential expression of FLS353 in breast tumor cells had not been previously demonstrated.

Cyclin-ubiquitin carrier protein E2-C is another gene over-expressed in breast cancer, which was discovered in this study. Previous studies have shown that when a dominant-negative form of the protein is over-expressed, the mammalian cells arrested in M phase and evidence was provided indicating that this mutant form of cyclin-ubiquitin carrier protein E2-C blocked the destruction of both cyclin A and B (see Townsley *et al., Proc Natl Acad Sci U S A* 94, 2362-7 (1997)).

The expression levels of the genes in Tables 4 and 5 are associated with various stages of infiltrating ductal carcinoma (Table 4) or infiltrating lobular carcinoma (Table 5). The Tables present the fold change value of expression in the particular disease state compared to normal breast tissue. The genes in these tables may be used alone, or in combination with those listed in Tables 1-3 in the methods, compositions, databases and computer systems of the invention.

Example 2: Diagnostic Subset of Breast Cancer Associated Genes

Table 1 lists the members of a diagnostic subset of genes selected by p-value. This group of genes can be used to differentiate between normal/benign and breast tumor tissue samples including two DCIS samples. Assays using these genes are capable of distinguishing between normal and tumor samples with near 100% efficiency (see Figure 6). Only 1 of the 33 samples shown was misclassified as a normal sample based on the gene

expression profile when this set of genes was used to analyze the 33 sample set (see Figure 7).

Figures 6 and 7 are three-dimensional plots displaying the relationship of variance derived from gene expression data obtained from patient samples. In Figure 6, normal tissue samples are displayed as darker spheres and the infiltrating ductal carcinoma tissue samples are the lighter spheres. The x-axis represents the first principal component that contains the greatest variance in data of 80%. The y-axis represents the second principal component of 4%. The z-axis represents the third principal component of 3%. Figure 7 displays the results obtained from a separate 33 sample set which is composed of new samples that have no relation to the 28 sample set utilized to discover the gene set of Table 1. Again, the x, y, and z-axes represent the first (63%), second (10%), and third principal components (6%), respectively.

The gene set of Table 1 can thus be used to distinguish normal from cancerous breast tissue.

Example 3: Myoepithelial and Luminal Cell Marker Genes Examined on a Global Scale

Previous studies have indicated that myoepithelial cells express both epithelial and smooth muscle gene expression markers while luminal epithelial cells fail to express these genes (see Lazard *et al., Proc Natl Acad Sci USA* 90, 999-1003 (1993)). Cluster analysis identified a group 35 fragments representing 31 genes into one highly correlative cluster and the combination of genes and ESTs are listed in Table 3.

Previous studies have indicated that calponin and myosin heavy chain are expressed in smooth muscle cells and myoepithelial cells while luminal epithelium lack the expression of these genes. Furthermore, the proteins are usually not expressed in invasive ductal carcinoma of the breast (Lazard, *et al.*, supra). Both calponin (fold change –11) and myosin heavy chain (fold change –10.8) were under-expressed in IDC. As indicated in Table 3, other genes associated with smooth muscle that were under-expressed such as smooth muscle gamma-actin, myosin light chain kinase, myosin, heavy polypeptide 11, and Leiomodin 1 and both mysoin polypeptide 11 and leiomodin 1 have not been previously reported to be under-expressed in breast cancer as compared to normal tissue samples.

The expression pattern represented in this particular cluster indicates that a preponderance of tissue samples diagnosed as infiltrating ductal carcinoma exhibit a luminal phenotype while myoepithelial cells were absent. More evidence to support this finding includes the under-expression of cytokeratins 5, 14, 15, and 17 in the tumor samples as

shown in Table 3. Normal myoepithelial cells express cytokeratins 5, 14, 15, and 17 and breast carcinoma cells do not (Trask *et al. Proc Natl Acad Sci USA* 87, 2319-2323 (1990)). A previous study has indicated that myoepithelial cells are present in normal, benign lesions, grade I infiltrating ductal carcinoma but are absent in carcinomas of grades II and III (Gusterson *et al. Cancer Res* 42, 4763-4770 (1982)).

In addition, components of the basal lamina such as laminin were under-expressed in the infiltrating ductal carcinoma relative to normal tissue samples (Table 3). Both laminin S B3 and laminin-related protein were under-expressed as indicated in Table 3. It has been reported that myoepithelial and basal lamina markers are useful in differentiating microinvasive from ductal carcinomas of the breast (Damiani *et al. Virchows Arch* 434, 227-234 (1999)).

The set of 35 fragments representing 31 genes as shown in Table 3 could distinguish between intraductal carcinoma and microinvasive DCIS tissue samples based on the disappearance of genes expressed in either basal lamina or myoepithelial cells. There is evidence in the literature that the collapse of the basement membrane as well as the disappearance of an intact myoepithelial cell layer occurs during the invasion process. A multi-gene screen utilizing either of these sets of genes can be used to differentiate between benign and invasive breast neoplasm based on the gene expression fingerprint elucidated in this study.

Figure 8 shows the results of PCA of the 91 sample set with all 35 fragments (representing 31 genes and ESTs) in Table 3. These results demonstrate that PCA using the genes in Table 3 is able to distinguish between non-invasive and invasive breast tissue samples. Figure 8 provides evidence that this group of genes is diagnostically useful for differentiating DCIS samples that are intraductal (non-invasive) from those containing microinvasion. As shown in Figure 8, this group of genes and ESTs is capable of differentiating between two subtypes of DCIS and may constitute a set that is a more sensitive predictor of a microinvasion phenotype.

Example 4: Discovery of Breast Tissue Specific Genes in IDC

Electronic northern (E-northern) analysis determines if a gene of interest is present in a tissue from a database of gene expression information, and if it is present, then at what levels. Expression levels were determined using a GeneChip set that evaluated the expression levels of 60,000 genes in each type of tissue from 28 different normal human tissues. Similar to multi-tissue northern blot analysis, E-northern analysis quickly

determines if a gene of interest is expressed in a particular tissue type and also at what level. E-northern analysis of multiple tissue samples can be evaluated and the determination of exactly how many samples of a particular group that express the gene of interest is tabulated and statistical analysis can be implemented. Multiple samples from the same tissue are not available at this time using conventional multi-tissue northern blot analysis.

The E-northern analysis can be used as a tool to discover tissue specific candidate therapeutic targets that are not over-expressed in tissues such as the liver, kidney, or heart. These tissue types often lead to detrimental side effects once drugs are developed and a first-pass screen to eliminate these targets early in the target discovery and validation process would be beneficial. Furthermore, different tissues have very unique gene expression profiles related to parameters such as proliferation, differentiation, or cell types contained in the tissue that can provide interesting clues into the biological roles of the ESTs.

E-northern analysis was performed for many of the genes clustered in Table 2. Analysis of the E-northerns revealed that most of the genes were expressed at elevated levels in the thymus. There is high rate of mitosis present in the thymus during T-lymphocyte maturation and many proliferation-associated genes are expressed at elevated levels such as CDC2, cyclin B1, and topoisomerase II alpha. Figure 1 displays the E-northern analysis for topoisomerase II alpha indicating elevated levels of expression in the thymus as compare to the other tissue types detected. Figure 2 shows the results of an E-Northern analysis of transcription factor ICBP90, implicated to be involved with topoisomearse II alpha expression. ICBP90 was also expressed at high levels relative to the other tissue types in the thymus (Figure 2). A study by Hopfner et al. indicated that adult thymus and fetal thymus contained the highest levels of ICBP90 using a 50-tissue RNA dot blot protocol (Hopfner *et al. Cancer Res* 60, 121-128 (2000)). Most of the genes contained in this cluster contained the highest levels of expression in the thymus.

Figure 3 shows the results of an E-Northern analysis of the monocarboxylate transporter 4 (MCT4; formerly known as MCT3) which was grouped with genes associated with proliferation. MCT4 is most evident in cells with a high glycolytic rate such as muscle, white blood cells, and tumor cells (Halestrap *et al.*, *Biochem J* 343 (Pt 2), 281-299 (1999)). A group of multi-tissue northern blots from a recent publication indicate that MCT4 is expressed at high levels in leukocytes but also other tissue types as well (Price *et al.*, *Biochem J* 329, 321-328 (1998)). Furthermore, electronic-northern analysis indicated high levels of MCT4 were expressed in blood and white blood cells (Figure 3).

A previously uncharacterized gene only expressed in breast tissue was identified from this study and an E-Northern analysis of the expression pattern of this gene is shown in Figure 4. The distribution pattern of the expression of the gene shows it be used as a marker for breast cancer. The E-northern analysis only displays tissues where the gene of interest is present at detectable levels and breast tissue was the only tissue that this particular gene was under-expressed by –4.2 fold in IDC making it particularly useful as a diagnostic marker.

Another gene that may be used as a diagnostic marker that was not present in a particular cluster is the secreted frizzled-related protein 1. This gene was under-expressed in IDC by –17.7 fold, and the E-northern analysis shown in Figure 5 indicates that it was expressed at greatest levels in breast tissue as well as in the cervix. Using the combination of clustering, fold-change analysis, and E-northern analysis on microarray data one skilled in the art can readily select additional therapeutic and diagnostic markers.

Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents and publications referred to in this application are herein incorporated by reference in their entirety.

Table 1: Top 50 by p-value

#	SeqID	Affy	Genbank	Description	Fold Change	p-values
1	1006	37892_at	J04177	Cluster Incl J04177:Human alpha-1 type XI collagen (COL11A1) mRNA, complete cds /cds=(161,5581) /gb=J04177 /gi=179729 /ug=Hs.82772 /len=6158	10.18941323	1.24E-12
2	278	35832_at	AB029000	Cluster Incl AB029000:Homo sapiens mRNA for KIAA1077 protein, partial cds /cds=(0,2456) /gb=AB029000 /gi=5689490 /ug=Hs.70823 /len=4834	4.243716901	2.469E-12
3	1227	38566_at	X60382	Cluster Incl X60382:H.sapiens COL10A1 gene for collagen (alpha-1 type X) /cds=(0,2042) /gb=X60382 /gi=30094 /ug=Hs.179729 /len=3198	9.164231149	4.719E-12
4	1226	38181_at	X57766	Cluster Incl X57766:Human stromelysin-3 mRNA /cds=(9,1475) /gb=X57766 /gi=456256 /ug=Hs.155324 /len=2247	13.96572736	5.309E-12
5	1159	1651_at	U73379	U73379 /FEATURE= /DEFINITION=HSU73379 Human cyclin-selective ubiquitin carrier protein mRNA, complete cds	4.802394237	5.8315E-11
6	1161	33143_s_at	U81800	Cluster Incl U81800:Homo sapiens monocarboxylate transporter (MCT3) mRNA, complete cds /cds=(62,1459) /gb=U81800 /gi=2463633 /ug=Hs.85838 /len=1982	0.07793742	6.2406E-11
7	296	34342_s_at	AF052124	Cluster Incl AF052124:Homo sapiens clone 23810 osteopontin mRNA, complete cds /cds=(87,989) /gb=AF052124 /gi=3360431 /ug=Hs.313 /len=1504	8.862541971	1.1789E-10
8	1008	31859_at	J05070	Cluster Incl J05070:Human type IV collagenase mRNA, complete cds /cds=(19,2142) /gb=J05070 /gi=177204 /ug=Hs.151738 /len=2334	4.66285568	1.68E-10
9	961	38116_at	D14657	Cluster Incl D14657:Human mRNA for KIAA0101 gene, complete cds /cds=(61,396) /gb=D14657 /gi=285938 /ug=Hs.81892 /len=836	0.17	2.1736E-10
10	1007	2092_s_at	J04765	J04765 /FEATURE= /DEFINITION=HUMOSTRO Human osteopontin mRNA, complete cds	4.119810176	3.9853E-10
11	277	39109_at	AB024704	Cluster Incl AB024704:Homo sapiens mRNA for fls353, complete cds /cds=(471,2714) /gb=AB024704 /gi=4589928 /ug=Hs.9329 /len=3403	0.228960682	6.59E-10

#	SeqID	Affy	Genbank	Description	Fold Change	p-values
12	1030	31720_s_at	M10905	Cluster Incl M10905:Human cellular fibronectin mRNA /cds=(0,2383) /gb=M10905 /gi=182696 /ug=Hs.118162 /len=2384	9.431588747	7.4333E-10
13	1240	35474_s_at	Y15915	Cluster Incl Y15915:Homo sapiens mRNA for chimaeric transcript of collagen type 1 alpha 1 and platelet derived growth factor beta, 1068 bp /cds=(0,1067) /gb=Y15915 /gi=3288486 /ug=Hs.172928 /len=1068	10.43	7.7763E-10
14	82	38432_at	AA203213	Cluster Incl AA203213:zx57e04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-446622 /clone_end=5" /gb=AA203213 /gi=1798923 /ug=Hs.833 /len=879"	5.975488989	9.3518E-10
15	1059	33338_at	M97936	Cluster Incl M97936:Human transcription factor ISGF-3 mRNA sequence /cds=UNKNOWN /gb=M97936 /gi=475254 /ug=Hs.21486 /len=2607	6.152409861	1.10E-09
16	1021	40161_at	L32137	Cluster Incl L32137:Human germline oligomeric matrix protein (COMP) mRNA, complete cds /cds=(25,2298) /gb=L32137 /gi=602449 /ug=Hs.1584 /len=2439	0.068952382	1.5685E-09
17	892	32190_at	AL050118	Cluster Incl AL050118:Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201) /cds=(0,936) /gb=AL050118 /gi=4884143 /ug=Hs.184641 /len=2621	0.139391318	1.5906E-09
18	105	34778_at	AA418080	Cluster Incl AA418080:zv97h07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-767773 /clone_end=3" /gb=AA418080 /gi=2079881 /ug=Hs.3972 /len=543"	0.047728145	1.7499E-09
19	1057	40619_at	M91670	Cluster Incl M91670:Human ubiquitin carrier protein (E2-EPF) mRNA, complete cds /cds=(59,736) /gb=M91670 /gi=181915 /ug=Hs.174070 /len=890	7.363245733	2.013E-09
20	83	40412_at	AA203476	Cluster Incl AA203476:zx55e01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-446424 /clone_end=5" /gb=AA203476 /gi=1799203 /ug=Hs.159626 /len=828"	8.54	2.0933E-09
21	1025	37985_at	L37747	Cluster Incl L37747:Homo sapiens lamin B1 gene /cds=(340,2100) /gb=L37747 /gi=576839 /ug=Hs.89497 /len=2849	0.233878866	2.11E-09

#	SeqID	Affy	Genbank	Description	Fold Change	p-values
22	1034	1107_s_at	M13755	M13755 /FEATURE=mRNA /DEFINITION=HUMIFN15K Human interferon-induced 17-kDa/15-kDa protein mRNA, complete cds	7.935291557	2.35E-09
23	1221	40195_at	X14850	Cluster Incl X14850:Human H2A.X mRNA encoding histone H2A.X /cds=(73,504) /gb=X14850 /gi=31972 /ug=Hs.147097 /len=1585	4.329038319	2.42E-09
24	1224	40690_at	X54942	Cluster Incl X54942:H.sapiens ckshs2 mRNA for Cks1 protein homologue /cds=(95,334) /gb=X54942 /gi=29978 /ug=Hs.83758 /len=612	0.233804467	2.6578E-09
25	1057	893_at	M91670	M91670 /FEATURE= /DEFINITION=HUME2EPI Human ubiquitin carrier protein (E2-EPF) mRNA, complete cds	0.16	2.8399E-09
26	1010	41400_at	K02581	Cluster Incl K02581:Human thymidine kinase mRNA, complete cds /cds=(57,761) /gb=K02581 /gi=339708 /ug=Hs.105097 /len=1421	0.284181885	3.1699E-09
27	444	40145_at	AI375913	Cluster Incl AI375913:tc14c08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2063822 /clone_end=3" /gb=AI375913 /gi=4175903 /ug=Hs.156346 /len=916"	6.816530863	3.56E-09
28	303	35995_at	AF067656	Cluster Incl AF067656:Homo sapiens ZW10 interactor Zwint mRNA, complete cds /cds=(24,857) /gb=AF067656 /gi=3901271 /ug=Hs.42650 /len=1639	10.36	4.0319E-09
29	205	39395_at	AA704137	Cluster Incl AA704137:ag47g01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1119984 /clone_end=3" /gb=AA704137 /gi=2714055 /ug=Hs.125359 /len=923"	0.103783146	4.2586E-09
30	1027	904_s_at	L47276	L47276 /FEATURE=UTR#1 /DEFINITION=HUMTOPATR Homo sapiens (cell line HL-60) alpha topoisomerase truncated-form mRNA, 3"UTR	4.690939862	5.41E-09

#	SeqID	Affy	Genbank	Description	Fold Change	p-values
31	91	39969_at	AA255502	Cluster Incl AA255502:zr85b06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-682451 /clone_end=5" /gb=AA255502 /gi=1892406 /ug=Hs.46423 /len=348"	0.222082398	5.4948E-09
32	1136	38414_at	U05340	Cluster Incl U05340:Human p55CDC mRNA, complete cds /cds=(110,1609) /gb=U05340 /gi=468031 /ug=Hs.82906 /len=1686	0.0564074	5.77E-09
33	1216	31719_at	X02761	Cluster Incl X02761:Human mRNA for fibronectin (FN precursor) /cds=(0,6987) /gb=X02761 /gi=31396 /ug=Hs.118162 /len=7680	0.145966282	5.79E-09
34	1160	34715_at	U74612	Cluster Incl U74612:Human hepatocyte nuclear factor 3/fork head homolog 11A (HFH-11A) mRNA complete cds /cds=(114,2519) /gb=U74612 /gi=1842252 /ug=Hs.239 /len=3474	0.075355998	5.93E-09
35	1043	34736_at	M25753	Cluster Incl M25753:Human cyclin B mRNA, 3 end /cds=UNKNOWN /gb=M25753 /gi=181243 /ug=Hs.23960 /len=1452"	7.624017858	5.98E-09
36	1002	32305_at	J03464	Cluster Incl J03464:Human collagen alpha-2 type I mRNA, complete cds, clone pHCOL2A1 /cds=(469,4569) /gb=J03464 /gi=179595 /ug=Hs.179573 /len=5416	7.973012437	6.70E-09
37	1222	38112_g_at	X15998	Cluster Incl X15998:H.sapiens mRNA for the chondroitin sulphate proteoglycan versican, V1 splice variant; precursor peptide /cds=(266,7495) /gb=X15998 /gi=37662 /ug=Hs.81800 /len=8224	0.273622601	6.7E-09
38	279	40162_s_at	AC003107	Cluster Incl AC003107:Human DNA from chromosome 19-specific cosmid R30064 containing the COMP gene, genomic sequence /cds=(0,2453) /gb=AC003107 /gi=2623749 /ug=Hs.1584 /len=2454	0.139924253	7.063E-09
39	1041	1577_at	M23263	M23263 /FEATURE= /DEFINITION=HUMARB Human androgen receptor mRNA, complete cds	12.37	7.3252E-09
40	276	41812_s_at	AB020713	Cluster Incl AB020713:Homo sapiens mRNA for KIAA0906 protein, partial cds /cds=(0,2772) /gb=AB020713 /gi=4240300 /ug=Hs.56966 /len=4217	0.184984291	8.5667E-09

#	SeqID	Affy	Genbank	Description	Fold Change	p-values
41	1155	33371_s_at	U59877	Cluster Incl U59877:Human low-Mr GTP-binding protein (RAB31) mRNA, complete cds /cds=(60,644) /gb=U59877 /gi=1388194 /ug=Hs.223025 /len=907	4.165483399	8.99E-09
42	307	33730_at	AF095448	Cluster Incl AF095448:Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds /cds=(99,1172) /gb=AF095448 /gi=4063889 /ug=Hs.194691 /len=2288	0.216723881	9.64E-09
43	756	32609_at	AI885852	Cluster Incl AI885852:wl62d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2429487 /clone_end=3" /gb=AI885852 /gi=5591016 /ug=Hs.795 /len=580"	0.292506358	1.0442E-08
44	1044	1371_s_at	M29874	M29874 /FEATURE= /DEFINITION=HUMCYP2BB Human cytochrome P450-IIB (hIIB1) mRNA, complete cds	3.425226104	1.1081E-08
45	1036	910_at	M15205	M15205 /FEATURE=cds /DEFINITION=HUMTKRA Human thymidine kinase gene, complete cds, with clustered Alu repeats in the introns	8.270850261	1.1279E-08
46	281	41583_at	AC004770	Cluster Incl AC004770:Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene /cds=(2644,3786) /gb=AC004770 /gi=3212836 /ug=Hs.4756 /len=4522	0.054106026	1.2153E-08
47	1233	35174_i_at	X70940	Cluster Incl X70940:H.sapiens mRNA for elongation factor 1 alpha-2 /cds=(83,1474) /gb=X70940 /gi=38455 /ug=Hs.2642 /len=1755	0.17504844	1.4629E-08

Table 2: Final Chip A-B-C-D-E

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
1	1006	37892_at	J04177	collagen, type XI, alpha 1	Hs.82772	Cluster Incl J04177:Human alpha-1 type XI collagen (COL11A1) mRNA, complete cds /cds=(161,5581) /gb=J04177 /gi=179729 /ug=Hs.82772 /len=6158	12.80130327	9.03E-07
2	1227	38566_at	X60382	collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia)	Hs.179729	Cluster Incl X60382:H.sapiens COL10A1 gene for collagen (alpha-1 type X) /cds=(0,2042) /gb=X60382 /gi=30094 /ug=Hs.179729 /len=3198	7.973012437	6.70E-09
3	1226	38181_at	X57766	matrix metalloproteinase 11 (stromelysin 3)	Hs.155324	Cluster Incl X57766:Human stromelysin-3 mRNA /cds=(9,1475) /gb=X57766 /gi=456256 /ug=Hs.155324 /len=2247	7.957396249	2.35E-08
4	1159	1651_at	U73379	ubiquitin carrier protein E2-C	Hs.93002	U73379 /FEATURE= /DEFINITION=HSU73379 Human cyclin-selective ubiquitin carrier protein mRNA, complete cds	7.935291557	2.35E-09
5	1161	33143_s_at	U81800	solute carrier family 16 (monocarboxylic acid transporters), member 3	Hs.85838	Cluster Incl U81800:Homo sapiens monocarboxylate transporter (MCT3) mRNA, complete cds /cds=(62,1459) /gb=U81800 /gi=2463633 /ug=Hs.85838 /len=1982	7.624017858	5.98E-09
6	296	34342_s_at	AF052124	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	Hs.313	Cluster Incl AF052124:Homo sapiens clone 23810 osteopontin mRNA, complete cds /cds=(87,989) /gb=AF052124 /gi=3360431 /ug=Hs.313 /len=1504	7.205250917	1.32E-04
7	1008	31859_at	J05070	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)	Hs.151738	Cluster Incl J05070:Human type IV collagenase mRNA, complete cds /cds=(19,2142) /gb=J05070 /gi=177204 /ug=Hs.151738 /len=2334	6.987016934	1.33E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
8	1007	2092_s_at	J04765	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	Hs.313	J04765 /FEATURE= /DEFINITION=HUMOSTRO Human osteopontin mRNA, complete cds	6.188665921	1.20E-04
9	277	39109_at	AB024704	chromosome 20 open reading frame 1	Hs.9329	Cluster Incl AB024704:Homo sapiens mRNA for fls353, complete cds /cds=(471,2714) /gb=AB024704 /gi=4589928 /ug=Hs.9329 /len=3403	6.152409861	1.10E-09
10	1030	31720_s_at	M10905	fibronectin 1	Hs.118162	Cluster Incl M10905:Human cellular fibronectin mRNA /cds=(0,2383) /gb=M10905 /gi=182696 /ug=Hs.118162 /len=2384	6.01925663	1.72E-04
11	1240	35474_s_at	Y15915	collagen, type I, alpha 1	Hs.172928	Cluster Incl Y15915:Homo sapiens mRNA for chimaeric transcript of collagen type 1 alpha 1 and platelet derived growth factor beta, 1068 bp /cds=(0,1067) /gb=Y15915 /gi=3288486 /ug=Hs.172928 /len=1068	5.903615342	1.76E-02
12	1059	33338_at	M97936	signal transducer and activator of transcription 1, 91kD	Hs.21486	Cluster Incl M97936:Human transcription factor ISGF-3 mRNA sequence /cds=UNKNOWN /gb=M97936 /gi=475254 /ug=Hs.21486 /len=2607	5.34214829	1.69E-07
13	1021	40161_at	L32137	cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple)	Hs.1584	Cluster Incl L32137:Human germline oligomeric matrix protein (COMP) mRNA, complete cds /cds=(25,2298) /gb=L32137 /gi=602449 /ug=Hs.1584 /len=2439	5.267240726	6.09E-06
14	1057	40619_at	M91670	ubiquitin carrier protein	Hs.174070	Cluster Incl M91670:Human ubiquitin carrier protein (E2-EPF) mRNA, complete cds /cds=(59,736) /gb=M91670 /gi=181915 /ug=Hs.174070 /len=890	4.694613277	2.18E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
15	83	40412_at	AA203476	pituitary tumor-transforming 1	Hs.252587	Cluster Incl AA203476:zx55e01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-446424 /clone_end=5" /gb=AA203476 /gi=1799203 /ug=Hs.159626 /len=828"	4.690939862	5.41E-09
16	1025	37985_at	L37747	lamin B1	Hs.89497	Cluster Incl L37747:Homo sapiens lamin B1 gene /cds=(340,2100) /gb=L37747 /gi=576839 /ug=Hs.89497 /len=2849	4.66285568	1.68E-10
17	1034	1107_s_at	M13755	interferon-stimulated protein, 15 kDa	Hs.833	M13755 /FEATURE=mRNA /DEFINITION=HUMIFN15K Human interferon-induced 17-kDa/15-kDa protein mRNA, complete cds	4.621425831	1.97E-06
18	1221	40195_at	X14850	H2A histone family, member X	Hs.147097	Cluster Incl X14850:Human H2A.X mRNA encoding histone H2A.X /cds=(73,504) /gb=X14850 /gi=31972 /ug=Hs.147097 /len=1585	4.485125913	3.67E-07
19	1224	40690_at	X54942	CDC28 protein kinase 2	Hs.83758	Cluster Incl X54942:H.sapiens ckshs2 mRNA for Cks1 protein homologue /cds=(95,334) /gb=X54942 /gi=29978 /ug=Hs.83758 /len=612	4.465375169	1.59E-08
20	1010	41400_at	K02581	thymidine kinase 1, soluble	Hs.105097	Cluster Incl K02581:Human thymidine kinase mRNA, complete cds /cds=(57,761) /gb=K02581 /gi=339708 /ug=Hs.105097 /len=1421	4.357390421	9.67E-08
21	303	35995_at	AF067656	ZW10 interactor	Hs.42650	Cluster Incl AF067656:Homo sapiens ZW10 interactor Zwint mRNA, complete cds /cds=(24,857) /gb=AF067656 /gi=3901271 /ug=Hs.42650 /len=1639	4.165483399	8.99E-09
22	1058	AFFX-HUMISGF3A/M97935_MA_at	M97935	signal transducer and activator of transcription 1, 91kD	Hs.21486	M97935 Homo sapiens transcription factor ISGF-3 mRNA, complete cds (_5, _MA, MB, _3 represent transcript regions 5 prime, MiddleA, MiddleB, and 3 prime respectively)	4.09	0.00077416
23	1027	904_s_at	L47276			L47276 /FEATURE=UTR#1 /DEFINITION=HUMTOPATR Homo sapiens (cell line HL-60) alpha topoisomerase truncated form mRNA, 3"UTR	4.002408289	1.88E-07

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
24	1136	38414_at	U05340	CDC20 (cell division cycle 20, S. cerevisiae, homolog)	Hs.82906	Cluster Incl U05340:Human p55CDC mRNA, complete cds /cds=(110,1609) /gb=U05340 /gi=468031 /ug=Hs.82906 /len=1686	3.870563686	1.06E-06
25	1216	31719_at	X02761	fibronectin 1	Hs.118162	Cluster Incl X02761:Human mRNA for fibronectin (FN precursor) /cds=(0,6987) /gb=X02761 /gi=31396 /ug=Hs.118162 /len=7680	3.855167487	2.48E-06
26	1160	34715_at	U74612	forkhead box M1	Hs.239	Cluster Incl U74612:Human hepatocyte nuclear factor-3/fork head homolog 11A (HFH-11A) mRNA complete cds /cds=(114,2519) /gb=U74612 /gi=1842252 /ug=Hs.239 /len=3474	3.813256493	2.95E-07
27	1043	34736_at	M25753	cyclin B1	Hs.23960	Cluster Incl M25753:Human cyclin B mRNA, 3 end /cds=UNKNOWN /gb=M25753 /gi=181243 /ug=Hs.23960 /len=1452"	3.80895841	2.60E-08
28	1002	32305_at	J03464	collagen, type I, alpha 2	Hs.179573	Cluster Incl J03464:Human collagen alpha-2 type I mRNA, complete cds, clone pHCOL2A1 /cds=(469,4569) /gb=J03464 /gi=179595 /ug=Hs.179573 /len=5416	3.800908625	4.11E-03
29	1222	38112_g_at	X15998	chondroitin sulfate proteoglycan 2 (versican)	Hs.81800	Cluster Incl X15998:H.sapiens mRNA for the chondroitin sulphate proteoglycan versican, V1 splice-variant; precursor peptide /cds=(266,7495) /gb=X15998 /gi=37662 /ug=Hs.81800 /len=8224	3.796503387	1.28E-05
30	279	40162_s_at	AC003107	cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple)	Hs.1584	Cluster Incl AC003107:Human DNA from chromosome 19-specific cosmid R30064 containing the COMP gene, genomic sequence /cds=(0,2453) /gb=AC003107 /gi=2623749 /ug=Hs.1584 /len=2454	3.781923678	3.71E-04

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
31	1041	1577_at	M23263	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)	Hs.99915	M23263 /FEATURE= /DEFINITION=HUMARB Human androgen receptor mRNA, complete cds	3.74871763	9.37E-05
32	1155	33371_s_at	U59877	RAB31, member RAS oncogene family	Hs.223025	Cluster Incl U59877:Human low-Mr GTP-binding protein (RAB31) mRNA, complete cds /cds=(60,644) /gb=U59877 /gi=1388194 /ug=Hs.223025 /len=907	3.620640004	1.57E-07
33	307	33730_at	AF095448	retinoic acid induced 3	Hs.194691	Cluster Incl AF095448:Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds /cds=(99,1172) /gb=AF095448 /gi=4063889 /ug=Hs.194691 /len=2288	3.607432569	1.35E-04
34	1044	1371_s_at	M29874	cytochrome P450, subfamily IIB (phenobarbital-inducible)	Hs.1360	M29874 /FEATURE= /DEFINITION=HUMCYP2BB Human cytochrome P450-IIB (hIIB1) mRNA, complete cds	3.556183255	5.17E-03
35	1036	910_at	M15205	thymidine kinase 1, soluble	Hs.105097	M15205 /FEATURE=cds /DEFINITION=HUMTKRA Human thymidine kinase gene, complete cds, with clustered Alu repeats in the introns	3.539960818	1.67E-05
36	281	41583_at	AC004770			Cluster Incl AC004770:Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene /cds=(2644,3786) /gb=AC004770 /gi=3212836 /ug=Hs.4756 /len=4522	3.437302377	9.47E-08
37	1233	35174_i_at	X70940	eukaryotic translation elongation factor 1 alpha 2	Hs.2642	Cluster Incl X70940:H.sapiens mRNA for elongation factor 1 alpha-2 /cds=(83,1474) /gb=X70940 /gi=38455 /ug=Hs.2642 /len=1755	3.435786237	3.03E-03
38	1231	425_at	X67325	interferon, alpha-inducible protein 27	Hs.278613	X67325 /FEATURE=cds /DEFINITION=HSP27 H.sapiens p27 mRNA	3.427509519	1.22E-03

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
39	1144	37302_at	U30872	centromere protein F (350/400kD, mitosin)	Hs.77204	Cluster Incl U30872:Human mitosin mRNA, complete cds /cds=(72,9413) /gb=U30872 /gi=1000093 /ug=Hs.77204 /len=10189	3.42481014	4.57E-07
40	1046	38404_at	M55153	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	Hs.8265	Cluster Incl M55153:Human transglutaminase (TGase) mRNA, complete cds /cds=(135,2198) /gb=M55153 /gi=339520 /ug=Hs.8265 /len=3257	3.411920822	1.19E-03
41	1215	AFFX-HSAC07/X00351_M_st	X00351	actin, beta	Hs.180952	X00351 Human mRNA for beta-actin (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	3.381535863	0.00448894
42	1033	38428_at	M13509	matrix metalloproteinase 1 (interstitial collagenase)	Hs.83169	Cluster Incl M13509:Human skin collagenase mRNA, complete cds /cds=(68,1477) /gb=M13509 /gi=180664 /ug=Hs.83169 /len=1970	3.370961478	9.83E-04
43	1005	37200_at	J04162	Fc fragment of IgG, low affinity IIIa, receptor for (CD16)	Hs.176663	Cluster Incl J04162:Human leukocyte IgG receptor (Fc-gamma-R) mRNA, complete cds /cds=(17,718) /gb=J04162 /gi=183036 /ug=Hs.763 /len=1977	3.349219771	2.37E-06
44	1234	37219_at	X72755	monokine induced by gamma interferon	Hs.77367	Cluster Incl X72755:H.sapiens Humig mRNA /cds=(39,416) /gb=X72755 /gi=311375 /ug=Hs.77367 /len=2545	3.329472506	5.97E-04
45	972	39677_at	D80008	KIAA0186 gene product	Hs.36232	Cluster Incl D80008:Human mRNA for KIAA0186 gene, complete cds /cds=(94,684) /gb=D80008 /gi=1136431 /ug=Hs.36232 /len=3248	3.328306522	5.87E-05
46	1043	1945_at	M25753	cyclin B1	Hs.23960	M25753 /FEATURE=mRNA /DEFINITION=HUMCYCB Human cyclin B mRNA, 3" end	3.295678907	5.63E-08
47	1054	32186_at	M80244	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	Hs.184601	Cluster Incl M80244:Human E16 mRNA, complete cds /cds=(310,1035) /gb=M80244 /gi=181907 /ug=Hs.184601 /len=3984	3.289545724	9.38E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
48	1053	37741_at	M77836	pyrroline-5-carboxylate reductase 1	Hs.79217	Cluster Incl M77836:Human pyrroline 5-carboxylate reductase mRNA, complete cds /cds=(11,970) /gb=M77836 /gi=189497 /ug=Hs.79217 /len=1792	3.247818871	2.25E-05
49	1049	36879_at	M63193	endothelial cell growth factor 1 (platelet-derived)	Hs.73946	Cluster Incl M63193:Human platelet-derived endothelial cell growth factor mRNA, complete cds /cds=(123,1571) /gb=M63193 /gi=189700 /ug=Hs.73946 /len=1587	3.190855222	4.06E-07
50	1158	37920_at	U70370	paired-like homeodomain transcription factor 1	Hs.84136	Cluster Incl U70370:Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds /cds=(111,1055) /gb=U70370 /gi=1870670 /ug=Hs.84136 /len=2049	3.147501909	6.11E-04
51	1149	37141_at	U39840	hepatocyte nuclear factor 3, alpha	Hs.105440	Cluster Incl U39840:Human hepatocyte nuclear factor-3 alpha (HNF-3 alpha) mRNA, complete cds /cds=(87,1508) /gb=U39840 /gi=1066121 /ug=Hs.105440 /len=2872	3.044487778	5.33E-04
52	1020	38763_at	L29254	sorbitol dehydrogenase	Hs.878	Cluster Incl L29254:Human (clone P1-5) L-iditol-2 dehydrogenase gene /cds=(137,1210) /gb=L29254 /gi=808013 /ug=Hs.878 /len=2519	3.044067136	1.78E-04
53	1219	1803_at	X05360	cell division cycle 2, G1 to S and G2 to M	Hs.184572	X05360 /FEATURE=cds /DEFINITION=HSCDC2 Human CDC2 gene involved in cell cycle control	3.036676875	7.75E-07
54	285	39690_at	AF002282	alpha-actinin-2-associated LIM protein	Hs.135281	Cluster Incl AF002282:Homo sapiens alpha-actinin-2 associated LIM protein mRNA, alternatively spliced product, complete cds /cds=(46,996) /gb=AF002282 /gi=3138923 /ug=Hs.135281 /len=1347	0.327422466	0.000054
55	1153	1527_s_at	U50527		Hs.22174	U50527 /FEATURE= /DEFINITION=HSU50527 Human BRCA2 region, mRNA sequence CG018	0.326731583	0.00000608

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
56	284	36890_at	AF001691	periplakin	Hs.74304	Cluster Incl AF001691:Homo sapiens 195 kDa cornified envelope precursor mRNA, complete cds /cds=(90,5360) /gb=AF001691 /gi=3168845 /ug=Hs.74304 /len=6227	0.326719388	0.0000229
57	1164	823_at	U84487	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)	Hs.80420	U84487 /FEATURE= /DEFINITION=HSU84487 Human CX3C chemokine precursor, mRNA, alternatively spliced, complete cds	0.326431324	0.000191
58	973	38049_g_at	D84110	RNA-binding protein gene with multiple splicing	Hs.80248	Cluster Incl D84110:Homo sapiens mRNA for RBP-MS/type 4, complete cds /cds=(566,1156) /gb=D84110 /gi=1669552 /ug=Hs.80248 /len=1594	0.323566748	0.0001
59	963	41120_at	D14686	aminomethyltransferase (glycine cleavage system protein T)	Hs.102	Cluster Incl D14686:Human gene for glycine cleavage system T-protein /cds=(145,1356) /gb=D14686 /gi=994760 /ug=Hs.102 /len=2119	0.323306977	2.84E-08
60	1001	33871_s_at	J02876	folate receptor 2 (fetal)	Hs.24194	Cluster Incl J02876:Human placental folate binding protein mRNA, complete cds /cds=(262,1029) /gb=J02876 /gi=182413 /ug=Hs.24194 /len=1211	0.323187581	0.000642
61	1120	851_s_at	S62539	insulin receptor substrate 1	Hs.96063	S62539 /FEATURE= /DEFINITION=S62539 insulin receptor substrate-1 [human, skeletal muscle, mRNA, 5828 nt]	0.323178779	0.00000552
62	1230	33263_at	X67098	rTS beta protein	Hs.180433	Cluster Incl X67098:H.sapiens rTS alpha mRNA containing four open reading frames /cds=UNKNOWN /gb=X67098 /gi=475908 /ug=Hs.180433 /len=1817	0.321819387	0.0000133
63	1154	34403_at	U58516	milk fat globule-EGF factor 8 protein	Hs.3745	Cluster Incl U58516:Human breast epithelial antigen BA46 mRNA, complete cds /cds=(60,1223) /gb=U58516 /gi=1381161 /ug=Hs.3745 /len=1934	0.3197207	0.000834

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
64	1169	37724_at	V00568	v-myc avian myelocytomatosis viral oncogene homolog	Hs.79070	Cluster Incl V00568:Human mRNA encoding the c-myc oncogene /cds=(558,1877) /gb=V00568 /gi=34815 /ug=Hs.79070 /len=2121	0.319370936	0.000387
65	1040	39385_at	M22324	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	Hs.1239	Cluster Incl M22324:Human aminopeptidase N/CD13 mRNA encoding aminopeptidase N, complete cds /cds=(120,3023) /gb=M22324 /gi=178535 /ug=Hs.1239 /len=3477	0.317801655	0.00529
66	292	41470_at	AF027208	prominin (mouse)-like 1	Hs.112360	Cluster Incl AF027208:Homo sapiens AC133 antigen mRNA, complete cds /cds=(37,2634) /gb=AF027208 /gi=2688948 /ug=Hs.112360 /len=3794	0.314829644	0.00523
67	958	770_at	D00632	glutathione peroxidase 3 (plasma)	Hs.172153	D00632 /FEATURE= /DEFINITION=HUMGSHPXA Homo sapiens mRNA for glutathione peroxidase, complete cds	0.313476219	0.000012
68	1018	668_s_at	L22524	matrix metalloproteinase 7 (matrilysin, uterine)	Hs.2256	L22524 /FEATURE=expanded_cds /DEFINITION=HUMMATRY06 Human matrilysin gene, exon 6 and complete cds	0.313295747	0.0224
69	1244	36917_at	Z26653	laminin, alpha 2 (merosin, congenital muscular dystrophy)	Hs.75279	Cluster Incl Z26653:H.sapiens mRNA for laminin M chain (merosin) /cds=(49,9381) /gb=Z26653 /gi=438055 /ug=Hs.75279 /len=9534	0.312357015	0.0000881
70	1016	279_at	L13740	nuclear receptor subfamily 4, group A, member 1	Hs.1119	L13740 /FEATURE= /DEFINITION=HUMTR3A Human TR3 orphan receptor mRNA, complete cds	0.31152273	0.000764

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
71	305	38339_at	AF082868	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase)	Hs.9667	Cluster Incl AF082868:Homo sapiens gamma butyrobetaine hydroxylase (BBH) mRNA, complete cds /cds=(66,1229) /gb=AF082868 /gi=3746804 /ug=Hs.9667 /len=1584	0.310894189	0.0000193
72	290	37251_s_at	AF016004	glycoprotein M6B	Hs.5422	Cluster Incl AF016004:Homo sapiens m6b1 mRNA, complete cds /cds=(254,1051) /gb=AF016004 /gi=3387766 /ug=Hs.78361 /len=1616	0.308897008	0.00000415
73	1239	32025_at	Y11306	transcription factor 7-like 2 (T-cell specific, HMG-box)	Hs.285857	Cluster Incl Y11306:Homo sapiens mRNA for hTCF-4 /cds=(307,2097) /gb=Y11306 /gi=4469251 /ug=Hs.154485 /len=2444	0.306961223	0.000274
74	1135	863_g_at	U04313	protease inhibitor 5 (maspin)	Hs.55279	U04313 /FEATURE= /DEFINITION=HSU04313 Human maspin mRNA, complete cds	0.303827048	0.000239
75	1242	34301_r_at	Z19574	keratin 17	Hs.2785	Cluster Incl Z19574:H.sapiens gene for cytokeratin 17 /cds=(64,1362) /gb=Z19574 /gi=30378 /ug=Hs.2785 /len=1518	0.303503697	0.0000802
76	1143	39545_at	U22398	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	Hs.106070	Cluster Incl U22398:Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds /cds=(260,1210) /gb=U22398 /gi=790247 /ug=Hs.106070 /len=1511	0.300299695	1.85E-07
77	1035	35752_s_at	M15036	protein S (alpha)	Hs.64016	Cluster Incl M15036:Human vitamin K-dependent plasma protein S mRNA, complete cds /cds=(146,2176) /gb=M15036 /gi=190288 /ug=Hs.64016 /len=3309	0.297519832	7.42E-08
78	1028	32052_at	L48215	hemoglobin, beta	Hs.155376	Cluster Incl L48215:Homo sapiens beta-globin (HBB) gene, with a to c allele 28 bp 5 to exon 1, (J00179 bases 61971-63802) /cds=(50,493) /gb=L48215 /gi=1066772 /ug=Hs.155376 /len=626"	0.296769339	0.00149

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
79	298	36065_at	AF052389	LIM domain binding 2,polymyositis/scleroderma autoantigen 2 (100kD)	Hs.4980	Cluster Incl AF052389:Homo sapiens LIM domain binding protein (LDB1) mRNA, complete cds /cds=(254,1297) /gb=AF052389 /gi=3044065 /ug=Hs.4980 /len=2398	0.295641772	0.0000556
80	848	40475_at	AJ000388	calpain-like protease	Hs.169172	Cluster Incl AJ000388:Homo sapiens mRNA for calpain-like protease CANPX /cds=(182,2107) /gb=AJ000388 /gi=2274961 /ug=Hs.169172 /len=3615	0.29509428	0.00000184
81	1031	36247_f_at	M12272	alcohol dehydrogenase 1 (class I), alpha polypeptide,alcohol dehydrogenase 3 (class I), gamma polypeptide	Hs.2523	Cluster Incl M12272:Homo sapiens alcohol dehydrogenase class I gamma subunit (ADH3) mRNA, complete cds /cds=(80,1207) /gb=M12272 /gi=178147 /ug=Hs.2523 /len=1466	0.29444252	0.00999
82	1165	32168_s_at	U85267	Down syndrome critical region gene 1	Hs.184222	Cluster Incl U85267:Homo sapiens down syndrome candidate region 1 (DSCR1) gene, alternative exon 1, complete cds /cds=(84,677) /gb=U85267 /gi=2612867 /ug=Hs.184222 /len=2272	0.292877726	0.00000996
83	308	32043_at	AF098462	stanniocalcin 2	Hs.155223	Cluster Incl AF098462:Homo sapiens stanniocalcin-related protein mRNA, complete cds /cds=(134,1042) /gb=AF098462 /gi=4050037 /ug=Hs.155223 /len=2380	0.29048531	0.00688
84	851	36711_at	AL021977	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F	Hs.51305	Cluster Incl AL021977:bK447C4.1 (novel MAFF (v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F) LIKE protein) /cds=(0,494) /gb=AL021977 /gi=4914526 /ug=Hs.51305 /len=2128	0.2896161	8.07E-07
85	1243	38059_g_at	Z22865	dermatopontin	Hs.80552	Cluster Incl Z22865:H.sapiens dermatopontin mRNA, complete CDS /cds=(12,617) /gb=Z22865 /gi=311613 /ug=Hs.80552 /len=729	0.288749983	0.000483

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
86	1004	32583_at	J04111	v-jun avian sarcoma virus 17 oncogene homolog	Hs.78465	Cluster Incl J04111:Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1 /cds=(974,1969) /gb=J04111 /gi=186624 /ug=Hs.78465 /len=3336	0.288106064	0.00000058
87	1019	1898_at	L24203	ataxia-telangiectasia group D-associated protein	Hs.82237	L24203 /FEATURE= /DEFINITION=HUMDK Homo sapiens ataxia-telangiectasia group D-associated protein mRNA, complete cds	0.287855932	0.000216
88	274	33222_at	AB017365	frizzled (Drosophila) homolog 7	Hs.173859	Cluster Incl AB017365:Homo sapiens mRNA for frizzled-7, complete cds /cds=(61,1785) /gb=AB017365 /gi=3927886 /ug=Hs.173859 /len=3851	0.287831724	0.0000355
89	1232	1005_at	X68277	dual specificity phosphatase 1	Hs.171695	X68277 /FEATURE=cds /DEFINITION=HSCL100 H.sapiens CL 100 mRNA for protein tyrosine phosphatase	0.287696584	0.00679
90	1017	287_at	L19871	activating transcription factor 3	Hs.460	L19871 /FEATURE= /DEFINITION=HUMATF3X Human activating transcription factor 3 (ATF3) mRNA, complete cds	0.285399252	0.000174
91	1145	37908_at	U31384	guanine nucleotide binding protein 11	Hs.83381	Cluster Incl U31384:Human G protein gamma-11 subunit mRNA, complete cds /cds=(107,328) /gb=U31384 /gi=995920 /ug=Hs.83381 /len=622	0.283121329	0.0000231
92	270	36503_at	AB002409	small inducible cytokine subfamily A (Cys-Cys), member 21	Hs.57907	Cluster Incl AB002409:Homo sapiens mRNA for SLC, complete cds /cds=(58,462) /gb=AB002409 /gi=2335034 /ug=Hs.57907 /len=852	0.282677481	0.000495
93	1013	656_at	L08488	inositol polyphosphate-1-phosphatase	Hs.32309	L08488 /FEATURE= /DEFINITION=HUMINOS Human inositol polyphosphate 1-phosphatase mRNA, complete cds	0.281207961	0.00000039
94	1151	32847_at	U48959	myosin, light polypeptide kinase	Hs.211582	Cluster Incl U48959:Homo sapiens myosin light chain kinase (MLCK) mRNA, complete cds /cds=(119,5863) /gb=U48959 /gi=1377819 /ug=Hs.211582 /len=5926	0.279338963	0.000161

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
95	1120	41049_at	S62539	insulin receptor substrate 1	Hs.96063	Cluster Incl S62539:insulin receptor substrate-1 [human, skeletal muscle, mRNA, 5828 nt] /cds=(1020,4748) /gb=S62539 /gi=386256 /ug=Hs.96063 /len=5799	0.278228021	0.00000917
96	1143	1787_at	U22398	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	Hs.106070	U22398 /FEATURE= /DEFINITION=HSU22398 Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds	0.276610822	0.00000688
97	1138	36686_at	U07919	aldehyde dehydrogenase 6	Hs.75746	Cluster Incl U07919:Human aldehyde dehydrogenase 6 mRNA, complete cds /cds=(52,1590) /gb=U07919 /gi=995897 /ug=Hs.75746 /len=3442	0.273963608	0.000014
98	1147	36073_at	U35139	necdin (mouse) homolog	Hs.50130	Cluster Incl U35139:Human NECDIN related protein mRNA, complete cds /cds=(58,1023) /gb=U35139 /gi=1754970 /ug=Hs.50130 /len=1592	0.273622601	6.7E-09
99	1050	41772_at	M68840	monoamine oxidase A	Hs.183109	Cluster Incl M68840:Human monoamine oxidase A (MAOA) mRNA, complete cds /cds=(73,1656) /gb=M68840 /gi=187352 /ug=Hs.183109 /len=1949	0.26818697	0.0000349
100	306	39038_at	AF093118	fibulin 5	Hs.11494	Cluster Incl AF093118:Homo sapiens UP50 mRNA, complete cds /cds=(168,1514) /gb=AF093118 /gi=3676821 /ug=Hs.11494 /len=2019	0.267616256	4.33E-07
101	1139	36010_at	U10492	mesenchyme homeo box 1	Hs.438	Cluster Incl U10492:Human Mox1 protein (MOX1) mRNA, complete cds /cds=(29,793) /gb=U10492 /gi=505653 /ug=Hs.438 /len=2315	0.263585259	0.00000159
102	291	41106_at	AF022797	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	Hs.10082	Cluster Incl AF022797:Homo sapiens intermediate conductance calcium-activated potassium channel (hKCa4) mRNA, complete cds /cds=(396,1679) /gb=AF022797 /gi=2674355 /ug=Hs.10082 /len=2238	0.260058306	0.000228

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
103	1141	36929_at	U17760	laminin, beta 3 (nicein (125kD), kalinin (140kD), BM600 (125kD))	Hs.75517	Cluster Incl U17760:Human laminin S B3 chain (LAMB3) gene /cds=(399,3917) /gb=U17760 /gi=2182192 /ug=Hs.75517 /len=4213	0.260055335	4.12E-07
104	1060	216_at	M98539	prostaglandin D2 synthase (21kD, brain)	Hs.8272	M98539 /FEATURE=exon /DEFINITION=HUMPDS03 Human prostaglandin D2 synthase gene, exon 7	0.259339901	0.0000904
105	1191	39750_at	W61005	DHHC1 protein	Hs.14896	Cluster Incl W61005:zd29a11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-342044 /clone_end=3" /gb=W61005 /gi=1367764 /ug=Hs.14896 /len=786"	0.259264106	0.0000232
106	999	31525_s_at	J00153	hemoglobin, alpha 1	Hs.251577	Cluster Incl J00153:Human alpha globin gene cluster on chromosome 16- zeta gene /cds=(0,428) /gb=J00153 /gi=183794 /ug=Hs.182374 /len=429	0.258780062	0.0025
107	1156	31855_at	U61374	sushi-repeat-containing protein, X chromosome	Hs.15154	Cluster Incl U61374:Human novel protein with short consensus repeats of six cysteines mRNA, complete cds /cds=(41,1426) /gb=U61374 /gi=1778409 /ug=Hs.15154 /len=1800	0.258230155	0.00000113
108	1225	38737_at	X57025	insulin-like growth factor 1 (somatomedia C)	Hs.85112	Cluster Incl X57025:Human IGF-I mRNA for insulin-like growth factor I /cds=(166,627) /gb=X57025 /gi=33007 /ug=Hs.85112 /len=7236	0.257792937	0.000041
109	1037	41209_at	M15856	lipoprotein lipase	Hs.180878	Cluster Incl M15856:Human lipoprotein lipase mRNA, complete cds /cds=UNKNOWN /gb=M15856 /gi=187209 /ug=Hs.180878 /len=3549	0.256900234	0.00041
110	1214	32552_at	X00129	retinol-binding protein 4, interstitial	Hs.76461	Cluster Incl X00129:Human mRNA for retinol binding protein (RBP) /cds=(51,650) /gb=X00129 /gi=35896 /ug=Hs.76461 /len=882	0.256815942	0.00105

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
111	1150	36156_at	U41518	aquaporin 1 (channel-forming integral protein, 28kD)	Hs.74602	Cluster Incl U41518:Human channel-like integral membrane protein (AQP-1) mRNA, clone AQP-1-2344, partial cds /cds=(0,460) /gb=U41518 /gi=1314305 /ug=Hs.74602 /len=2344	0.256739005	0.000837
112	1238	41094_at	Y10179	prolactin-induced protein	Hs.99949	Cluster Incl Y10179:H.sapiens mRNA for prolactin-inducible protein /cds=(36,476) /gb=Y10179 /gi=2292895 /ug=Hs.99949 /len=576	0.251627664	0.0321
113	1011	37015_at	K03000	aldehyde dehydrogenase 1, soluble	Hs.76392	Cluster Incl K03000:Human aldehyde dehydrogenase 1 mRNA /cds=(0,1022) /gb=K03000 /gi=178399 /ug=Hs.76392 /len=1560	0.251471671	0.000106
114	1042	31687_f_at	M25079	hemoglobin, beta	Hs.155376	Cluster Incl M25079:Human sickle cell beta-globin mRNA, complete cds /cds=(0,443) /gb=M25079 /gi=179408 /ug=Hs.234764 /len=468	0.251434843	0.000998
115	1148	33756_at	U39447	amine oxidase, copper containing 3 (vascular adhesion protein 1)	Hs.198241	Cluster Incl U39447:Human placenta copper monamine oxidase mRNA, complete cds /cds=(160,2451) /gb=U39447 /gi=1399031 /ug=Hs.198241 /len=4023	0.250173978	0.000037
116	1225	1501_at	X57025	insulin-like growth factor 1 (somatomedia C)	Hs.85112	X57025 /FEATURE=mRNA /DEFINITION=HSIGFACI Human IGF-I mRNA for insulin-like growth factor I	0.249382262	0.0000523
117	1012	1897_at	L07594	transforming growth factor, beta receptor III (betaglycan, 300kD)	Hs.79059	L07594 /FEATURE= /DEFINITION=HUMTGFB3C Human transforming growth factor-beta type III receptor (TGF-beta) mRNA, complete cds	0.248516754	0.0000179
118	1137	32805_at	U05861	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	Hs.275374	Cluster Incl U05861:Human hepatic dihydrodiol dehydrogenase gene /cds=(26,997) /gb=U05861 /gi=487134 /ug=Hs.201967 /len=1222	0.242494771	0.000763

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
119	1162	36943_r_at	U81992	pleiomorphic adenoma gene-like 1	Hs.75825	Cluster Incl U81992:Homo sapiens C2H2 zinc finger protein PLAGL1 (PLAGL1) mRNA, complete cds /cds=(176,1411) /gb=U81992 /gi=3513452 /ug=Hs.75825 /len=2561	0.233878866	2.11E-09
120	1237	32610_at	X93510	LIM domain protein	Hs.79691	Cluster Incl X93510:H.sapiens mRNA for 37 kDa LIM domain protein /cds=(41,1027) /gb=X93510 /gi=1085021 /ug=Hs.79691 /len=1130	0.233549169	0.0000034
121	294	33700_at	AF039843	sprouty (Drosophila) homolog 2	Hs.18676	Cluster Incl AF039843:Homo sapiens Sprouty 2 (SPRY2) mRNA, complete cds /cds=(390,1337) /gb=AF039843 /gi=2809399 /ug=Hs.18676 /len=2117	0.231782987	3.37E-08
122	1014	38408_at	L10373	transmembrane 4 superfamily member 2	Hs.82749	Cluster Incl L10373:Human (clone CCG-B7) mRNA sequence /cds=UNKNOWN /gb=L10373 /gi=307287 /ug=Hs.82749 /len=1792	0.228960682	6.59E-10
123	960	774_g_at	D10667			D10667 /FEATURE= /DEFINITION=HUMMHCAAA Homo sapiens mRNA for smooth muscle myosin heavy chain, partial cds	0.228917694	0.000415
124	1146	36329_at	U33147	mammaglobin 1	Hs.46452	Cluster Incl U33147:Human mammaglobin mRNA, complete cds /cds=(60,341) /gb=U33147 /gi=1199595 /ug=Hs.46452 /len=503	0.226749627	0.031
125	1003	37863_at	J04076	early growth response 2 (Krox-20 (Drosophila) homolog)	Hs.1395	Cluster Incl J04076:Human early growth response 2 protein (EGR2) mRNA, complete cds /cds=(203,1423) /gb=J04076 /gi=181986 /ug=Hs.1395 /len=2700	0.225166891	3.52E-07
126	1241	31791_at	Y16961	tumor protein 63 kDa with strong homology to p53	Hs.137569	Cluster Incl Y16961:Homo sapiens mRNA for KET protein /cds=(27,2069) /gb=Y16961 /gi=3970716 /ug=Hs.137569 /len=4849	0.222238905	0.00000788
127	1152	39350_at	U50410	glypican 3	Hs.119651	Cluster Incl U50410:Human heparan sulphate proteoglycan (OCI5) mRNA, complete cds /cds=(144,1886) /gb=U50410 /gi=1245416 /ug=Hs.119651 /len=2269	0.220336613	0.0000975

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
128	1223	37765_at	X54162	leiomodin 1 (smooth muscle)	Hs.79386	Cluster Incl X54162:Human mRNA for a 64 Kd autoantigen expressed in thyroid and extra-ocular muscle /cds=(212,1930) /gb=X54162 /gi=28968 /ug=Hs.79386 /len=3849	0.218509986	0.00000138
129	1157	32239_at	U69263	matrilin 2	Hs.19368	Cluster Incl U69263:Human matrilin-2 precursor mRNA, partial cds /cds=(0,941) /gb=U69263 /gi=2072789 /ug=Hs.19368 /len=1033	0.216723881	9.64E-09
130	1026	39066_at	L38486	microfibrillar-associated protein 4	Hs.118223	Cluster Incl L38486:Human microfibril-associated glycoprotein 4 (MFAP4) mRNA, 3 end of cds /cds=(0,771) /gb=L38486 /gi=790816 /ug=Hs.118223 /len=1757"	0.216083178	0.0000527
131	1045	37187_at	M36820	GRO2 oncogene	Hs.75765	Cluster Incl M36820:Human cytokine (GRO-beta) mRNA, complete cds /cds=(74,397) /gb=M36820 /gi=183628 /ug=Hs.75765 /len=1110	0.207358276	0.0000209
132	1142	32666_at	U19495	stromal cell-derived factor 1	Hs.237356	Cluster Incl U19495:Human intercrine-alpha (hIRH) mRNA, complete cds /cds=(473,742) /gb=U19495 /gi=1754834 /ug=Hs.169672 /len=2244	0.206077576	0.00000443
133	1218	32275_at	X04470	secretory leukocyte protease inhibitor (antileukoproteinase)	Hs.251754	Cluster Incl X04470:Human mRNA for antileukoprotease (ALP) from cervix uterus /cds=(18,416) /gb=X04470 /gi=28638 /ug=Hs.169793 /len=594	0.202234909	0.000166
134	282	38995_at	AF000959	claudin 5 (transmembrane protein deleted in velocardiofacial syndrome)	Hs.110903	Cluster Incl AF000959:Homo sapiens transmembrane protein mRNA, complete cds /cds=(120,776) /gb=AF000959 /gi=2150012 /ug=Hs.110903 /len=1348	0.19705452	0.0000371
135	1015	37701_at	L13463	regulator of G-protein signalling 2, 24kD	Hs.78944	Cluster Incl L13463:Human helix-loop-helix basic phosphoprotein (G0S8) mRNA, complete cds /cds=(32,667) /gb=L13463 /gi=292054 /ug=Hs.78944 /len=1345	0.196869236	4.51E-07

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
136	1168	37149_s_at	U95626	lactotransferrin	Hs.347	Cluster Incl U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607	0.195015273	0.0108
137	1038	40488_at	M18533	dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272	Hs.169470	Cluster Incl M18533:Homo sapiens dystrophin (DMD) mRNA, complete cds /cds=UNKNOWN /gb=M18533 /gi=181856 /ug=Hs.169470 /len=13957	0.191432122	2.64E-10
138	295	36555_at	AF044311	synuclein, gamma (breast cancer-specific protein 1)	Hs.63236	Cluster Incl AF044311:Homo sapiens gamma-synuclein gene, complete cds /cds=(52,435) /gb=AF044311 /gi=3347841 /ug=Hs.63236 /len=708	0.19139473	0.000818
139	1023	37909_at	L34155	laminin, alpha 3 (nicein (150kD), kalinin (165kD), BM600 (150kD), epilegrin)	Hs.83450	Cluster Incl L34155:Homo sapiens laminin-related protein (LamA3) mRNA, complete cds /cds=(0,5141) /gb=L34155 /gi=551596 /ug=Hs.83450 /len=5433	0.187743879	4.71E-08
140	1051	38326_at	M69199	putative lymphocyte G0/G1 switch gene	Hs.95910	Cluster Incl M69199:Human G0S2 protein gene, complete cds /cds=(160,471) /gb=M69199 /gi=609453 /ug=Hs.95910 /len=863	0.187570884	0.00058
141	1024	41124_r_at	L35594	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	Hs.174185	Cluster Incl L35594:Human autotaxin mRNA, complete cds /cds=(49,2796) /gb=L35594 /gi=537905 /ug=Hs.174185 /len=3231	0.186647173	9.21E-08

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
142	1000	36681_at	J02611	apolipoprotein D	Hs.75736	Cluster Incl J02611:Human apolipoprotein D mRNA, complete cds /cds=(61,630) /gb=J02611 /gi=178840 /ug=Hs.75736 /len=809	0.186645351	0.00041
143	1056	41618_at	M91669	collagen, type XVII, alpha 1	Hs.117938	Cluster Incl M91669:Human Bullous pemphigoid autoantigen BP180 gene, 3 end /cds=(0,4598) /gb=M91669 /gi=179516 /ug=Hs.117938 /len=4669"	0.185170181	1.65E-07
144	1235	36042_at	X75958	neurotrophic tyrosine kinase, receptor, type 2	Hs.47860	Cluster Incl X75958:H.sapiens trkB mRNA for protein-tyrosine kinase /cds=(97,1530) /gb=X75958 /gi=473007 /ug=Hs.47860 /len=2224	0.185137314	9.59E-07
145	1024	41123_s_at	L35594	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	Hs.174185	Cluster Incl L35594:Human autotaxin mRNA, complete cds /cds=(49,2796) /gb=L35594 /gi=537905 /ug=Hs.174185 /len=3231	0.176679484	6.44E-07
146	1022	33902_at	L34041	glycerol-3-phosphate dehydrogenase 1 (soluble)	Hs.286116	Cluster Incl L34041:Homo sapiens L-glycerol-3 phosphate-NAD oxidoreductase mRNA, complete cds /cds=(29,1078) /gb=L34041 /gi=508486 /ug=Hs.25478 /len=1413	0.173326424	0.00000343
147	1016	280_g_at	L13740	nuclear receptor subfamily 4, group A, member 1	Hs.1119	L13740 /FEATURE= /DEFINITION=HUMTR3A Human TR3 orphan receptor mRNA, complete cds	0.173040601	0.0000486
148	966	40658_r_at	D45371	adipose most abundant gene transcript 1	Hs.80485	Cluster Incl D45371:Human apM1 mRNA for GS3109 (novel adipose specific collagen-like factor), complete cds /cds=(26,760) /gb=D45371 /gi=871886 /ug=Hs.80485 /len=4517	0.172026427	0.000161
149	301	32542_at	AF063002	four and a half LIM domains 1	Hs.239069	Cluster Incl AF063002:Homo sapiens LIM protein SLIMMER mRNA, complete cds /cds=(84,1055) /gb=AF063002 /gi=3859848 /ug=Hs.75329 /len=2042	0.168054499	0.00000205
150	1228	40375_at	X63741	early growth response 3	Hs.74088	Cluster Incl X63741:H.sapiens pilot mRNA /cds=(353,1516) /gb=X63741 /gi=35472 /ug=Hs.74088 /len=4272	0.163077134	0.00000359

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
151	1140	32648_at	U15979	delta-like homolog (Drosophila)	Hs.169228	Cluster Incl U15979:Human (dlk) mRNA, complete cds /cds=(173,1321) /gb=U15979 /gi=562105 /ug=Hs.169228 /len=1553	0.161923599	0.00506
152	1009	2094_s_at	K00650	v-fos FBJ murine osteosarcoma viral oncogene homolog	Hs.25647	K00650 /FEATURE=cds /DEFINITION=HUMFOS Human fos proto-oncogene (c-fos), complete cds	0.161859881	0.00282
153	1217	35730_at	X03350	alcohol dehydrogenase 2 (class I), beta polypeptide	Hs.4	Cluster Incl X03350:Human mRNA for alcohol dehydrogenase beta-1-subunit (ADH1-2 allele) /cds=(72,1199) /gb=X03350 /gi=28415 /ug=Hs.4 /len=2532	0.155156674	0.0000162
154	1229	36569_at	X64559	tetranectin (plasminogen-binding protein)	Hs.65424	Cluster Incl X64559:H.sapiens mRNA for tetranectin /cds=(93,701) /gb=X64559 /gi=37408 /ug=Hs.65424 /len=848	0.145966282	5.79E-09
155	293	36892_at	AF032108	integrin, alpha 7	Hs.74369	Cluster Incl AF032108:Homo sapiens integrin alpha-7 mRNA, complete cds /cds=(161,3574) /gb=AF032108 /gi=2897115 /ug=Hs.74369 /len=4061	0.143559713	0.00000648
156	1047	234_s_at	M57399	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	Hs.44	M57399 /FEATURE= /DEFINITION=HUMHBNF1 Human nerve growth factor (HBNF-1) mRNA, complete cds	0.138540058	0.0000201
157	1048	1736_at	M62402	insulin-like growth factor binding protein 6	Hs.274313	M62402 /FEATURE= /DEFINITION=HUMIGFBP4 Human insulin-like growth factor binding protein 6 (IGFBP6) mRNA, complete cds	0.137509192	0.00000235
158	1032	34637_f_at	M12963	alcohol dehydrogenase 1 (class I), alpha polypeptide	Hs.73843	Cluster Incl M12963:Human class I alcohol dehydrogenase (ADH1) alpha subunit mRNA, complete cds /cds=(72,1199) /gb=M12963 /gi=178089 /ug=Hs.73843 /len=1450	0.137096706	0.000768
159	271	37122_at	AB005293	perilipin	Hs.103253	Cluster Incl AB005293:Homo sapiens mRNA for perilipin, complete cds /cds=(124,1692) /gb=AB005293 /gi=3041770 /ug=Hs.103253 /len=2904	0.136296847	0.0000385

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
160	849	36018_at	AJ001183	SRY (sex determining region Y)-box 10	Hs.44317	Cluster Incl AJ001183:Homo sapiens mRNA for Sox10 protein /cds=(120,1520) /gb=AJ001183 /gi=2909359 /ug=Hs.44317 /len=2547	0.13521119	1.19E-07
161	1029	36669_at	L49169	FBJ murine osteosarcoma viral oncogene homolog B	Hs.75678	Cluster Incl L49169:Human G0S3 mRNA, complete cds /cds=(593,1609) /gb=L49169 /gi=1082037 /ug=Hs.75678 /len=3775	0.124249102	0.000082
162	283	767_at	AF001548	myosin, heavy polypeptide 11, smooth muscle	Hs.78344	AF001548 /FEATURE=mRNA /DEFINITION=HUAF001548 Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence	0.121953593	0.0000134
163	1055	40282_s_at	M84526	D component of complement (adipsin)	Hs.155597	Cluster Incl M84526:Human adipsin/complement factor D mRNA, complete cds /cds=(54,740) /gb=M84526 /gi=178625 /ug=Hs.155597 /len=1071	0.118530255	-9.26E-08
164	1166	38508_s_at	U89337	tenascin XA	Hs.283750	Cluster Incl U89337:Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds /cds=(0,12869) /gb=U89337 /gi=1841544 /ug=Hs.169886 /len=12870	0.118243196	9.15E-08
165	1039	613_at	M21389	keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)	Hs.195850	M21389 /FEATURE=mRNA /DEFINITION=HUMKER2A Human keratin type II (58 kD) mRNA, complete cds	0.116969229	0.000222
166	45	38430_at	AA128249	fatty acid binding protein 4, adipocyte	Hs.83213	Cluster Incl AA128249:zl29d09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-503345 /clone_end=5" /gb=AA128249 /gi=1688343 /ug=Hs.83213 /len=648"	0.108941232	0.000439

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
167	1167	40339_at	U95367	gamma-aminobutyric acid (GABA) A receptor, pi	Hs.70725	Cluster Incl U95367:Human GABA-A receptor pi subunit mRNA, complete cds /cds=(156,1478) /gb=U95367 /gi=2197000 /ug=Hs.70725 /len=3264	0.108244989	9.35E-07
168	1047	34820_at	M57399	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	Hs.44	Cluster Incl M57399:Human nerve growth factor (HBNF-1) mRNA, complete cds /cds=(395,901) /gb=M57399 /gi=292072 /ug=Hs.44 /len=1029	0.10121597	5.83E-07
169	1220	37582_at	X07696	keratin 15	Hs.80342	Cluster Incl X07696:Human mRNA for cytokeratin 15 /cds=(61,1431) /gb=X07696 /gi=34070 /ug=Hs.80342 /len=1709	0.097312672	0.000249
170	1052	40304_at	M69225	bullous pemphigoid antigen 1 (230/240kD)	Hs.620	Cluster Incl M69225:Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds /cds=UNKNOWN /gb=M69225 /gi=179522 /ug=Hs.620 /len=8930	0.096634153	0.00000084
171	288	37407_s_at	AF013570	myosin, heavy polypeptide 11, smooth muscle	Hs.78344	Cluster Incl AF013570:Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gi=2352944 /ug=Hs.78344 /len=2580	0.092826583	0.0000236
172	964	34203_at	D17408	calponin 1, basic, smooth muscle	Hs.21223	Cluster Incl D17408:Homo sapiens mRNA for calponin, complete cds /cds=(92,985) /gb=D17408 /gi=1783204 /ug=Hs.21223 /len=1517	0.091111614	2.66E-08
173	959	1197_at	D00654	actin, gamma 2, smooth muscle, enteric	Hs.77443	D00654 /FEATURE=cds /DEFINITION=HUMACTSG7 Homo sapiens gene for enteric smooth muscle gamma-actin, exon9, complete cds	0.090848213	3.51E-07
174	998	39052_at	J00124	keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)	Hs.117729	Cluster Incl J00124:Homo sapiens 50 kDa type I epidermal keratin gene, complete cds /cds=(61,1479) /gb=J00124 /gi=186704 /ug=Hs.117729 /len=1634	0.070781449	0.00000596

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
175	299	32521_at	AF056087	secreted frizzled-related protein 1	Hs.7306	Cluster Incl AF056087:Homo sapiens secreted frizzled related protein mRNA, complete cds /cds=(302,1243) /gb=AF056087 /gi=3033550 /ug=Hs.7306 /len=4458	0.0564074	5.77E-09
176	923	74989_at	AW007442	zinc finger protein homologous to Zfp92 in mouse	Hs.821	Cluster Incl. AW007442:wt55g06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2511418 /clone_end=3' /gb=AW007442 /gi=5856220 /ug=Hs.235961 /len=424'	7.73694268	0.00055334
177	843	80675_at	AI990026	v-myb avian myeloblastosis viral oncogene homolog-like 2	Hs.179718	Cluster Incl. AI990026:ws37c04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2499366 /clone_end=3' /gb=AI990026 /gi=5836907 /ug=Hs.239557 /len=452'	4.18	0.00136502
178	183	64695_at	AA614135	VLCS-H1 protein	Hs.49765	Cluster Incl. AA614135:no82f09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1113353 /clone_end=3' /gb=AA614135 /gi=2466269 /ug=Hs.49765 /len=564'	0.282343722	4.5016E-06
179	901	59253_at	AL118633	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	Hs.151678	Cluster Incl. AL118633:DKFZp761F0810_r1 Homo sapiens cDNA, 5 end /clone=DKFZp761F0810 /clone_end=5' /gb=AL118633 /gi=5924532 /ug=Hs.151678 /len=660'	3.871753195	0.00129495
180	411	91419_at	AI283888	ubiquitin specific protease 25	Hs.186961	Cluster Incl. AI283888:qk51f12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1872527 /clone_end=3' /gb=AI283888 /gi=3922121 /ug=Hs.153544 /len=420'	0.308362018	0.00039175
181	525	48513_at	AI589804	tweety (Drosophila) homolog 1	Hs.12828	Cluster Incl. AI589804:tm74e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2163884 /clone_end=3' /gb=AI589804 /gi=4598852 /ug=Hs.12828 /len=508'	0.227899817	2.7406E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
182	913	57034_at	AW003626	tubulin, beta, 4	Hs.159154	Cluster Incl. AW003626:wx34e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2545562 /clone_end=3' /gb=AW003626 /gi=5850542 /ug=Hs.234018 /len=707'	6.818460543	0.00017707
183	833	74593_at	AI973225	TTK protein kinase	Hs.169840	Cluster Incl. AI973225:wr53c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2491412 /clone_end=3' /gb=AI973225 /gi=5770051 /ug=Hs.233704 /len=399'	4.363660627	1.0421E-05
184	847	52238_s_at	AI990642	transforming, acidic coiled-coil containing protein 3	Hs.104019	Cluster Incl. AI990642:ws22g06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2497978 /clone_end=3' /gb=AI990642 /gi=5837523 /ug=Hs.233886 /len=591'	4.2443289	3.9817E-06
185	10	63346_at	AA026429	transcription factor	Hs.108106	Cluster Incl. AA026429:ze92a04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-366414 /clone_end=5' /gb=AA026429 /gi=1492330 /ug=Hs.108106 /len=479'	4.256819836	1.5585E-05
186	911	74096_at	AW003286	topoisomerase (DNA) II alpha (170kD)	Hs.270810	Cluster Incl. AW003286:wq65a02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2476106 /clone_end=3' /gb=AW003286 /gi=5850202 /ug=Hs.232126 /len=773'	9.431588747	7.4333E-10
187	208	90442_at	AA707213	topoisomerase (DNA) I	Hs.317	Cluster Incl. AA707213:zj32h06.s1 Homo sapiens cDNA, 3 end /clone=452027 /clone_end=3' /gb=AA707213 /gi=2717131 /ug=Hs.14319 /len=527'	5.50	0.00109754
188	488	57778_at	AI480357	thyroid hormone responsive SPOT14 (rat) homolog	Hs.91877	Cluster Incl. AI480357:tm51d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2161647 /clone_end=3' /gb=AI480357 /gi=4373525 /ug=Hs.91877 /len=830'	0.149624624	0.00022486
189	205	39395_at	AA704137	Thy-1 cell surface antigen	Hs.125359	Cluster Incl AA704137:ag47g01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1119984 /clone_end=3" /gb=AA704137 /gi=2714055 /ug=Hs.125359 /len=923"	4.122293677	6.75E-04

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
190	152	48101_at	AA527151	sterol-C5-desaturase (fungal ERG3, delta-5 desaturase)-like	Hs.184242	Cluster Incl. AA527151:ni07b08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-967287 /clone_end=3' /gb=AA527151 /gi=2269220 /ug=Hs.108977 /len=559'	3.418467862	0.00065669
191	585	43039_at	AI675177	SRY (sex determining region Y)-box 8	Hs.243678	Cluster Incl. AI675177:tm80g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2164472 /clone_end=3' /gb=AI675177 /gi=4875657 /ug=Hs.229620 /len=548'	0.284181885	3.1699E-09
192	854	91880_at	AL036753	SRY (sex determining region Y)-box 11	Hs.32964	Cluster Incl. AL036753:DKFZp564I0663_r1 Homo sapiens cDNA, 5 end /clone=DKFZp564I0663 /clone_end=5' /gb=AL036753 /gi=5927893 /ug=Hs.133482 /len=617'	6.66	0.00058351
193	800	78444_at	AI949433	sperm surface protein	Hs.129872	Cluster Incl. AI949433:wq11e08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2470982 /clone_end=3' /gb=AI949433 /gi=5741831 /ug=Hs.13562 /len=561'	0.31	3.4432E-06
194	412	63335_at	AI285531	sorting nexin 10	Hs.106260	Cluster Incl. AI285531:qu49b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1968079 /clone_end=3' /gb=AI285531 /gi=3923764 /ug=Hs.106260 /len=598'	4.206790316	2.6069E-05
195	980	49498_at	H10816	small protein effector 1 of Cdc42	Hs.22065	Cluster Incl. H10816:ym04e12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-46664 /clone_end=5' /gb=H10816 /gi=875636 /ug=Hs.22065 /len=660'	3.273076721	0.00051209
196	1077	65823_at	N45415	small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)	Hs.24395	Cluster Incl. N45415:yw97h06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-260219 /clone_end=5' /gb=N45415 /gi=1186581 /ug=Hs.24395 /len=647'	0.325281828	0.00133643
197	616	33790_at	AI720438	small inducible cytokine subfamily A (Cys-Cys), member 14	Hs.20144	Cluster Incl AI720438:as81g04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2335158 /clone_end=3" /gb=AI720438 /gi=5037694 /ug=Hs.20144 /len=550"	0.277326129	0.0000138

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
198	39	50094_at	AA102575	serum deprivation response (phosphatidylserine-binding protein)	Hs.26530	Cluster Incl. AA102575:zn42c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-550084 /clone_end=3' /gb=AA102575 /gi=1647767 /ug=Hs.26530 /len=589'	0.13254339	1.7128E-08
199	233	33272_at	AA829286	serum amyloid A1	Hs.181062	Cluster Incl AA829286:of08a01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1420488 /clone_end=3" /gb=AA829286 /gi=2902385 /ug=Hs.181062 /len=559"	0.147972137	0.000166
200	732	63580_at	AI832477	serologically defined colon cancer antigen 43	Hs.132792	Cluster Incl. AI832477:at69b10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2377243 /clone_end=3' /gb=AI832477 /gi=5454457 /ug=Hs.22386 /len=414'	0.279118305	5.5177E-07
201	729	62486_at	AI829385	semaphorin sem2	Hs.59729	Cluster Incl. AI829385:wk64e08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2420198 /clone_end=3' /gb=AI829385 /gi=5450056 /ug=Hs.59729 /len=480'	0.113932898	2.1786E-06
202	1213	78757_at	W92110	selenoprotein X	Hs.279623	Cluster Incl. W92110:zh48d06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-415307 /clone_end=5' /gb=W92110 /gi=1424473 /ug=Hs.239939 /len=582'	3.52	0.02422274
203	746	74815_at	AI864016	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	Hs.313	Cluster Incl. AI864016:wj53h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2406595 /clone_end=3' /gb=AI864016 /gi=5528123 /ug=Hs.234375 /len=511'	5.371729632	0.00029667
204	46	34319_at	AA131149	S100 calcium-binding protein P	Hs.2962	Cluster Incl AA131149:zo16d05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-587049 /clone_end=5" /gb=AA131149 /gi=1692640 /ug=Hs.2962 /len=464"	3.31996447	3.31E-03
205	844	57027_at	AI990405	retinoic acid induced 3	Hs.194691	Cluster Incl. AI990405:ws20h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2497795 /clone_end=3' /gb=AI990405 /gi=5837286 /ug=Hs.233881 /len=481'	5.815956961	8.0344E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
206	900	69473_r_at	AL110368	reelin	Hs.12246	Cluster Incl. AL110368:DKFZp564P1078_s1 Homo sapiens cDNA, 3 end /clone=DKFZp564P1078 /clone_end=3' /gb=AL110368 /gi=5865976 /ug=Hs.198353 /len=720'	0.18	4.5657E-06
207	61	91384_at	AA147088	ral guanine nucleotide dissociation stimulator	Hs.106185	Cluster Incl. AA147088:zo32c07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-588588 /clone_end=3' /gb=AA147088 /gi=1716461 /ug=Hs.106185 /len=688'	0.30	0.02812425
208	677	74300_at	AI799107	RAD54, S. cerevisiae, homolog of, B	Hs.128501	Cluster Incl. AI799107:we98h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2349171 /clone_end=3' /gb=AI799107 /gi=5364579 /ug=Hs.128501 /len=713'	3.28	0.00031747
209	895	44037_at	AL079372	RAD51 (S. cerevisiae) homolog (E coli RecA homolog)	Hs.23044	Cluster Incl. AL079372:DKFZp564H1178_s1 Homo sapiens cDNA, 3 end /clone=DKFZp564H1178 /clone_end=3' /gb=AL079372 /gi=5423266 /ug=Hs.23044 /len=655'	4.031107597	4.4105E-06
210	620	46683_at	AI739117	RAB6 interacting, kinesin-like (rabkinesin6)	Hs.73625	Cluster Incl. AI739117:wi18c04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2390598 /clone_end=3' /gb=AI739117 /gi=5101098 /ug=Hs.73625 /len=762'	6.276196882	2.9782E-08
211	737	57173_at	AI858626	pyruvate kinase, muscle	Hs.198281	Cluster Incl. AI858626:wl40g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2427416 /clone_end=3' /gb=AI858626 /gi=5512242 /ug=Hs.30807 /len=617'	0.26701338	1.3574E-05
212	420	48647_at	AI304339	pyruvate dehydrogenase kinase, isoenzyme 4	Hs.8364	Cluster Incl. AI304339:qo58g10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1912770 /clone_end=3' /gb=AI304339 /gi=3988028 /ug=Hs.8364 /len=614'	0.183592799	2.9836E-06
213	81	45799_at	AA195614	protein regulator of cytokinesis 1	Hs.5101	Cluster Incl. AA195614:zr37b09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-665561 /clone_end=5' /gb=AA195614 /gi=1783791 /ug=Hs.5101 /len=635'	5.975488989	9.3518E-10

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
214	726	86573_at	AI828396	prohibitin	Hs.75323	Cluster Incl. AI828396:wk84e07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2422116 /clone_end=3' /gb=AI828396 /gi=5449067 /ug=Hs.201574 /len=465'	0.31	1.0797E-05
215	625	55569_at	AI741776	procollagen C-endopeptidase enhancer 2	Hs.8944	Cluster Incl. AI741776:wg22g10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2365890 /clone_end=3' /gb=AI741776 /gi=5110064 /ug=Hs.8944 /len=641'	0.181794989	5.5208E-05
216	173	84574_r_at	AA593830	PRO0611 protein	Hs.163833	Cluster Incl. AA593830:nn17b11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1084125 /clone_end=3' /gb=AA593830 /gi=2408508 /ug=Hs.163833 /len=405'	3.638706185	0.03570463
217	745	65700_at	AI863965	PRO0529 protein	Hs.279898	Cluster Incl. AI863965:wj54b08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2406615 /clone_end=3' /gb=AI863965 /gi=5527996 /ug=Hs.15285 /len=601'	0.158415546	0.00261362
218	607	45294_at	AI697470	polymeric immunoglobulin receptor	Hs.205126	Cluster Incl. AI697470:tq08h01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2208241 /clone_end=3' /gb=AI697470 /gi=4985370 /ug=Hs.205126 /len=494'	0.062026919	7.8961E-05
219	874	71106_i_at	AL044906	polycystic kidney disease 1 (autosomal dominant)	Hs.75813	Cluster Incl. AL044906:DKFZp434K183_r1 Homo sapiens cDNA, 5 end /clone=DKFZp434K183 /clone_end=5' /gb=AL044906 /gi=5433103 /ug=Hs.211647 /len=485'	0.19	0.00044405
220	492	90494_at	AI492388	poly(A)-binding protein, nuclear 1	Hs.117176	Cluster Incl. AI492388:ti27d10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2131699 /clone_end=3' /gb=AI492388 /gi=4393391 /ug=Hs.145011 /len=477'	0.14	9.7327E-07
221	161	91095_s_at	AA535819	PMEPA1 protein	Hs.83883	Cluster Incl. AA535819:nj79e01.s1 Homo sapiens cDNA /clone=IMAGE-998712 /gb=AA535819 /gi=2280072 /ug=Hs.238355 /len=522	5.25	6.0939E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
222	824	57266_r_at	AI971679	pleiomorphic adenoma gene-like 1	Hs.75825	Cluster Incl. AI971679:wq88b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2479081 /clone_end=3' /gb=AI971679 /gi=5768505 /ug=Hs.233974 /len=573'	0.325587729	5.9471E-05
223	698	62196_at	AI815028	pleckstrin homology-like domain, family A, member 1	Hs.82101	Cluster Incl. AI815028:wk70b07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2420725 /clone_end=3' /gb=AI815028 /gi=5426243 /ug=Hs.5285 /len=492'	0.224464715	0.00024055
224	705	59010_at	AI818248	phospholipid scramblase 4	Hs.182538	Cluster Incl. AI818248:wk77f02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2421435 /clone_end=3' /gb=AI818248 /gi=5437327 /ug=Hs.182538 /len=793'	0.285584964	5.6196E-05
225	143	63017_at	AA521373	phosphoinositol 3-phosphate binding protein-1	Hs.9469	Cluster Incl. AA521373:aa77g02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-826994 /clone_end=3' /gb=AA521373 /gi=2261916 /ug=Hs.9469 /len=525'	0.257023901	0.00023065
226	924	80604_at	AW007566	phosphoenolpyruvate carboxykinase 1 (soluble)	Hs.1872	Cluster Incl. AW007566:wt02e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2506300 /clone_end=3' /gb=AW007566 /gi=5856429 /ug=Hs.239193 /len=624'	0.28	0.00627388
227	1128	90033_at	T66157	phosphodiesterase 2A, cGMP-stimulated	Hs.154437	Cluster Incl. T66157:yc77d06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-22165 /clone_end=3' /gb=T66157 /gi=675202 /ug=Hs.238001 /len=418'	0.133294383	1.9181E-06
228	738	77546_at	AI859144	odd Oz/ten-m homolog 2 (Drosophila, mouse)	Hs.173560	Cluster Incl. AI859144:wl67a10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2429946 /clone_end=3' /gb=AI859144 /gi=5512760 /ug=Hs.173560 /len=546'	0.25	2.4915E-05
229	804	78518_at	AI951185	nuclear receptor subfamily 2, group F, member 1	Hs.144630	Cluster Incl. AI951185:wx64e12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2548462 /clone_end=3' /gb=AI951185 /gi=5743495 /ug=Hs.144630 /len=787'	0.29	2.4435E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
230	435	63877_r_at	AI355848	nuclear factor I/X (CCAAT-binding transcription factor)	Hs.35841	Cluster Incl. AI355848:qu02d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1963601 /clone_end=3' /gb=AI355848 /gi=4096001 /ug=Hs.239464 /len=715'	0.199980315	0.00020188
231	790	49666_s_at	AI935353	nuclear autoantigenic sperm protein (histone-binding)	Hs.243886	Cluster Incl. AI935353:wo82d12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2461847 /clone_end=3' /gb=AI935353 /gi=5674223 /ug=Hs.234669 /len=532'	3.316200333	0.00307749
232	486	72236_at	AI479933	NK-2 (Drosophila) homolog B	Hs.159623	Cluster Incl. AI479933:tm73b08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2163735 /clone_end=3' /gb=AI479933 /gi=4373101 /ug=Hs.223933 /len=465'	4.64	6.6167E-05
233	1188	82657_f_at	W48800	ninein	Hs.44054	Cluster Incl. W48800:zc44f03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-325181 /clone_end=5' /gb=W48800 /gi=1336949 /ug=Hs.167297 /len=451'	0.117240353	0.000479
234	114	72026_g_at	AA427578	neurotrophin 5 (neurotrophin 4/5)	Hs.266902	Cluster Incl. AA427578:zw54b07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-773845 /clone_end=3' /gb=AA427578 /gi=2112006 /ug=Hs.220975 /len=525'	0.17504844	1.4629E-08
235	328	56809_at	AI052524	neurobeachin	Hs.3821	Cluster Incl. AI052524:oz27f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1676581 /clone_end=3' /gb=AI052524 /gi=3308515 /ug=Hs.4799 /len=537'	0.262530591	6.7348E-06
236	105	34778_at	AA418080	NeuAc-alpha-2,3-Gal-beta-1,3-GalNAc-alpha-2, 6-sialyltransferase alpha2,6-sialyltransferase	Hs.3972	Cluster Incl AA418080:zv97h07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-767773 /clone_end=3" /gb=AA418080 /gi=2079881 /ug=Hs.3972 /len=543"	4.698983711	4.93E-06
237	630	55457_at	AI742260	NADPH oxidase 4	Hs.93847	Cluster Incl. AI742260:wg39g10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367522 /clone_end=3' /gb=AI742260 /gi=5110548 /ug=Hs.93847 /len=789'	3.809930405	5.3066E-07

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
238	150	46276_at	AA526844	myosin, light polypeptide kinase	Hs.211582	Cluster Incl. AA526844:ni92d10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-984307 /clone_end=3' /gb=AA526844 /gi=2268913 /ug=Hs.77310 /len=669'	0.32670528	4.4362E-07
239	283	32582_at	AF001548	myosin, heavy polypeptide 11, smooth muscle	Hs.78344	Cluster Incl AF001548:Human Chromosome 16 BAC clone CIT987SK-A-815A9 /cds=(0,5573) /gb=AF001548 /gi=2104552 /ug=Hs.78344 /len=6428	0.168769332	0.0000139
240	697	46743_s_at	AI814178	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 7	Hs.239663	Cluster Incl. AI814178:wk63e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2420106 /clone_end=3' /gb=AI814178 /gi=5425393 /ug=Hs.234582 /len=408'	0.288946314	0.00225117
241	1093	58494_r_at	N78139	muscle-specific protein	Hs.42346	Cluster Incl. N78139:yv73d07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-248365 /clone_end=5' /gb=N78139 /gi=1240840 /ug=Hs.239825 /len=656'	4.848524211	0.00151003
242	1069	59624_g_at	N27428	M-phase phosphoprotein 1	Hs.240	Cluster Incl. N27428:yx81h09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-268193 /clone_end=3' /gb=N27428 /gi=1141909 /ug=Hs.221178 /len=407'	3.068295724	1.1301E-05
243	111	41771_g_at	AA420624	monoamine oxidase A	Hs.183109	Cluster Incl AA420624:nc61c12.r1 Homo sapiens cDNA /clone=IMAGE-745750 /gb=AA420624 /gi=2094502 /ug=Hs.183109 /len=533	0.23811529	0.0000045
244	222	84934_at	AA776393	metallocarboxypeptidase CPX-1	Hs.177536	Cluster Incl. AA776393:ah16g09.s1 Homo sapiens cDNA, 3 end /clone=1156864 /clone_end=3' /gb=AA776393 /gi=2835727 /ug=Hs.177536 /len=602'	0.23	0.00267462
245	127	39271_at	AA461365	melanoma inhibitory activity,ras-related GTP-binding protein 4b	Hs.279771	Cluster Incl AA461365:zx70e07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-796836 /clone_end=5" /gb=AA461365 /gi=2186485 /ug=Hs.237742 /len=591"	0.246437105	0.0000502

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
246	829	75254_at	AI972357	matrilin 2	Hs.19368	Cluster Incl. AI972357:wr37c09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2489872 /clone_end=3' /gb=AI972357 /gi=5769183 /ug=Hs.237874 /len=524'	0.196704294	6.1415E-06
247	480	78644_at	AI459139	lymphocyte-specific protein 1	Hs.56729	Cluster Incl. AI459139:tj65e05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2146400 /clone_end=3' /gb=AI459139 /gi=4311718 /ug=Hs.235590 /len=519'	0.12	1.9615E-06
248	819	74541_at	AI969879	low density lipoprotein related protein 1 (alpha-2-macroglobulin receptor)	Hs.89137	Cluster Incl. AI969879:wq76f05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2477217 /clone_end=3' /gb=AI969879 /gi=5766697 /ug=Hs.233610 /len=329'	0.307354772	0.00253759
249	1176	74835_r_at	W22091	ligase I, DNA, ATP-dependent	Hs.1770	Cluster Incl. W22091:61F10 Homo sapiens cDNA /clone=(not-directional) /gb=W22091 /gi=1298924 /ug=Hs.234460 /len=637	4.366999247	0.00110724
250	976	48950_at	F36908	Kv channel-interacting protein 2	Hs.97044	Cluster Incl. F36908:HSPD34832 Homo sapiens cDNA /clone=sH5-000021-0/A10 /gb=F36908 /gi=4822534 /ug=Hs.97044 /len=408	0.247555921	0.0005914
251	699	47113_at	AI815057	Kruppel-like factor 5 (intestinal)	Hs.84728	Cluster Incl. AI815057:wk70e06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2420770 /clone_end=3' /gb=AI815057 /gi=5426272 /ug=Hs.86559 /len=484'	0.214230439	0.00014885
252	416	48587_at	AI290876	Kruppel-like factor 4 (gut)	Hs.182965	Cluster Incl. AI290876:qm14b02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1881771 /clone_end=3' /gb=AI290876 /gi=3933650 /ug=Hs.182965 /len=643'	0.322163154	8.7304E-05
253	2	51160_at	AA004208	kinesin family member 4A	Hs.279766	Cluster Incl. AA004208:zh97c02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-429218 /clone_end=3' /gb=AA004208 /gi=1448403 /ug=Hs.27437 /len=665'	3.542386026	6.1228E-07

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
254	1194	49599_at	W68504	KIAA1479 protein	Hs.191098	Cluster Incl. W68504:zd36b01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-342697 /clone_end=5' /gb=W68504 /gi=1377374 /ug=Hs.21288 /len=613'	0.189411148	3.2252E-06
255	250	88138_at	AA912409	KIAA1396 protein	Hs.230188	Cluster Incl. AA912409:ol23a07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1524276 /clone_end=3' /gb=AA912409 /gi=3051801 /ug=Hs.192271 /len=379'	0.317853152	0.00090706
256	302	63393_at	AF063500	KIAA1368 protein	Hs.263395	Cluster Incl. AF063500:AF063500 Homo sapiens cDNA /clone=HA0052 /gb=AF063500 /gi=5080920 /ug=Hs.17424 /len=652	0.28929478	0.00048007
257	334	76253_at	AI073544	KIAA1240 protein	Hs.62576	Cluster Incl. AI073544:ov45e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1640282 /clone_end=3' /gb=AI073544 /gi=3400188 /ug=Hs.120703 /len=481'	3.778012983	0.00894957
258	350	52793_at	AI097463	KIAA1130 protein	Hs.21035	Cluster Incl. AI097463:qb90a04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1707342 /clone_end=3' /gb=AI097463 /gi=3447045 /ug=Hs.21035 /len=464'	0.231260722	9.936E-05
259	986	90920_at	H19400	KIAA1130 protein	Hs.21035	Cluster Incl. H19400:ym46g07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-51511 /clone_end=5' /gb=H19400 /gi=888095 /ug=Hs.21035 /len=488'	0.20	4.1926E-05
260	278	35832_at	AB029000	KIAA1077 protein	Hs.70823	Cluster Incl AB029000:Homo sapiens mRNA for KIAA1077 protein, partial cds /cds=(0,2456) /gb=AB029000 /gi=5689490 /ug=Hs.70823 /len=4834	10.18941323	1.24E-12
261	276	41812_s_at	AB020713	KIAA0906 protein	Hs.56966	Cluster Incl AB020713:Homo sapiens mRNA for KIAA0906 protein, partial cds /cds=(0,2772) /gb=AB020713 /gi=4240300 /ug=Hs.56966 /len=4217	3.635450964	1.69E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
262	58	65593_at	AA142956	KIAA0781 protein	Hs.42676	Cluster Incl. AA142956:zl43g02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-504722 /clone_end=3' /gb=AA142956 /gi=1712334 /ug=Hs.239142 /len=640'	0.247630859	9.6801E-06
263	203	68283_r_at	AA701619	KIAA0614 protein	Hs.7314	Cluster Incl. AA701619:zi41f11.s1 Homo sapiens cDNA, 3 end /clone=433389 /clone_end=3' /gb=AA701619 /gi=2704784 /ug=Hs.190382 /len=398'	0.33	0.04190137
264	273	39382_at	AB011089	KIAA0517 protein	Hs.12372	Cluster Incl AB011089:Homo sapiens mRNA for KIAA0517 protein, partial cds /cds=(0,2380) /gb=AB011089 /gi=3043557 /ug=Hs.12372 /len=6740	0.226047115	2.62E-08
265	269	39544_at	AB002351	KIAA0353 protein	Hs.10587	Cluster Incl AB002351:Human mRNA for KIAA0353 gene, partial cds /cds=(0,4125) /gb=AB002351 /gi=2224646 /ug=Hs.10587 /len=6651	0.075355998	5.93E-09
266	207	91405_at	AA706612	KIAA0210 gene product	Hs.115740	Cluster Incl. AA706612:ah26c02.s1 Homo sapiens cDNA, 3 end /clone=1239938 /clone_end=3' /gb=AA706612 /gi=2716530 /ug=Hs.115740 /len=949'	0.22	5.5307E-05
267	961	38116_at	D14657	KIAA0101 gene product	Hs.81892	Cluster Incl D14657:Human mRNA for KIAA0101 gene, complete cds /cds=(61,396) /gb=D14657 /gi=285938 /ug=Hs.81892 /len=836	6.816530863	3.56E-09
268	962	34760_at	D14664	KIAA0022 gene product	Hs.2441	Cluster Incl D14664:Human mRNA for KIAA0022 gene, complete cds /cds=(184,696) /gb=D14664 /gi=285952 /ug=Hs.2441 /len=3694	0.325833287	0.0000146
269	731	62998_at	AI831452	keratin 6B	Hs.111758	Cluster Incl. AI831452:wj49b03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2406125 /clone_end=3' /gb=AI831452 /gi=5452123 /ug=Hs.91539 /len=597'	0.3274967	0.01054263

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
270	518	79663_at	AI566193	iroquois homeobox protein 4	Hs.196927	Cluster Incl. AI566193:tq69f02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2214075 /clone_end=3' /gb=AI566193 /gi=4524645 /ug=Hs.196927 /len=393'	0.18	0.00012792
271	557	63628_at	AI655781	interleukin 7 receptor	Hs.237868	Cluster Incl. AI655781:tt39h04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2243191 /clone_end=3' /gb=AI655781 /gi=4739760 /ug=Hs.237868 /len=806'	3.175184161	0.0007796
272	928	89921_at	AW008322	interleukin 11 receptor, alpha	Hs.64310	Cluster Incl. AW008322:wv53d07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990848 /clone_end=3' /gb=AW008322 /gi=5857100 /ug=Hs.234145 /len=556'	0.146596341	7.6279E-07
273	82	38432_at	AA203213	interferon-stimulated protein, 15 kDa	Hs.833	Cluster Incl AA203213:zx57e04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-446622 /clone_end=5" /gb=AA203213 /gi=1798923 /ug=Hs.833 /len=879"	5.51416519	1.23E-05
274	826	73285_i_at	AI971748	integrin, beta 4	Hs.85266	Cluster Incl. AI971748:wr07f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2480871 /clone_end=3' /gb=AI971748 /gi=5768574 /ug=Hs.236704 /len=841'	0.25	0.01689309
275	850	40775_at	AL021786	integral membrane protein 2A	Hs.17109	Cluster Incl AL021786:Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs /cds=(0,680) /gb=AL021786 /gi=2853186 /ug=Hs.17109 /len=1389	0.171820134	1.29E-07
276	942	64305_s_at	AW022660	insulin-like growth factor 1 (somatomedia C)	Hs.85112	Cluster Incl. AW022660:df42a02.y1 Homo sapiens cDNA, 5 end /clone=IMAGE-2485899 /clone_end=5' /gb=AW022660 /gi=5876190 /ug=Hs.236002 /len=505'	0.310324615	0.0007917
277	14	56338_at	AA031286	insulin receptor substrate 2	Hs.143648	Cluster Incl. AA031286:zk13b04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-470383 /clone_end=3' /gb=AA031286 /gi=1501241 /ug=Hs.10494 /len=512'	0.223459008	6.2389E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
278	852	41536_at	AL022726	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	Hs.34853	Cluster Incl AL022726:Human DNA sequence from clone 625H18 on chromosome 6p22.2-23. Contains the gene for ID4 Helix-loop-helix DNA binding protein and part of an alternatively spliced novel gene. Contains ESTs, STSs, GSSs and putative CpG islands /cds=(368,853) /gb=AL022726 /gi=3676217 /ug=Hs.34853 /len=3859	0.309888618	0.0000161
279	67	63798_at	AA152276	indolethylamine N-methyltransferase	Hs.204038	Cluster Incl. AA152276:zl06e06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-491554 /clone_end=5' /gb=AA152276 /gi=1721679 /ug=Hs.204038 /len=618'	0.316720069	0.0016656
280	570	37006_at	AI660656	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	Hs.76325	Cluster Incl AI660656:wf23c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2351436 /clone_end=3" /gb=AI660656 /gi=4764239 /ug=Hs.76325 /len=522"	0.23941203	0.000411
281	696	75127_f_at	AI813866	immunoglobulin heavy contant alpha 1	Hs.283305	Cluster Incl. AI813866:wk61b03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2419853 /clone_end=3' /gb=AI813866 /gi=5425081 /ug=Hs.236913 /len=539'	0.302724058	0.00034019
282	727	58869_i_at	AI828404	immunoglobulin heavy constant gamma 3 (Gm marker)	Hs.140	Cluster Incl. AI828404:wk84f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2422117 /clone_end=3' /gb=AI828404 /gi=5449075 /ug=Hs.236937 /len=601'	10.30345974	1.7517E-05
283	935	64258_f_at	AW016235	hypothetical protein PRO2160	Hs.112844	Cluster Incl. AW016235:UI-H-BI0p-abl-a-06-0-UI.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2712083 /clone_end=3' /gb=AW016235 /gi=5864992 /ug=Hs.234283 /len=438'	0.1264716	3.744E-08

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
284	195	60810_at	AA651733	hypothetical protein MPMGp800C04260Q 003	Hs.21861	Cluster Incl. AA651733:ns67b07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-1188661 /clone_end=5' /gb=AA651733 /gi=2583385 /ug=Hs.21861 /len=515'	0.297383187	2.1399E-07
285	1063	49633_at	N21131	hypothetical protein HES6	Hs.42949	Cluster Incl. N21131:yx52g04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-265398 /clone_end=3' /gb=N21131 /gi=1126301 /ug=Hs.233612 /len=571'	3.983397486	4.8443E-05
286	9	50223_at	AA020743	hypothetical protein from EUROIMAGE 363668	Hs.271277	Cluster Incl. AA020743:ze63c11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-363668 /clone_end=3' /gb=AA020743 /gi=1484525 /ug=Hs.234026 /len=626'	0.047728145	1.7499E-09
287	144	54742_at	AA521440	hypothetical protein FLJ20701	Hs.169764	Cluster Incl. AA521440:aa69c11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-826196 /clone_end=3' /gb=AA521440 /gi=2261983 /ug=Hs.169764 /len=583'	0.289179561	5.2039E-08
288	406	47427_at	AI276023	hypothetical protein FLJ20539	Hs.118552	Cluster Incl. AI276023:qw08h12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1990535 /clone_end=3' /gb=AI276023 /gi=3898297 /ug=Hs.11388 /len=476'	3.336721416	0.00014333
289	167	91394_at	AA563601	hypothetical protein FLJ20489	Hs.267368	Cluster Incl. AA563601:ng47c07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-937932 /clone_end=3' /gb=AA563601 /gi=2335240 /ug=Hs.109297 /len=436'	0.32	0.00241384
290	231	56634_at	AA813827	hypothetical protein FLJ20354	Hs.133260	Cluster Incl. AA813827:ny14a09.s1 Homo sapiens cDNA /clone=IMAGE-1271704 /gb=AA813827 /gi=2883423 /ug=Hs.87807 /len=422	3.188106939	1.8721E-05
291	371	70129_r_at	AI149537	hypothetical protein FLJ20320	Hs.263081	Cluster Incl. AI149537:qc70g02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1714994 /clone_end=3' /gb=AI149537 /gi=3678006 /ug=Hs.203401 /len=527'	4.36	0.00187809

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
292	76	50280_at	AA181060	hypothetical protein FLJ20163	Hs.92254	Cluster Incl. AA181060:zp66h06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-625211 /clone_end=3' /gb=AA181060 /gi=1764543 /ug=Hs.239302 /len=607'	3.437531315	0.00010396
293	656	74539_g_at	AI766666	hypothetical protein FLJ20159	Hs.161554	Cluster Incl. AI766666:wi02e05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2389088 /clone_end=3' /gb=AI766666 /gi=5233175 /ug=Hs.233608 /len=518'	4.739571659	0.00090349
294	213	43439_at	AA741298	hypothetical protein FLJ11252	Hs.23495	Cluster Incl. AA741298:oc86a07.s1 Homo sapiens cDNA /clone=IMAGE-1356564 /gb=AA741298 /gi=2779890 /ug=Hs.23495 /len=530	3.646875259	6.097E-08
295	445	53962_at	AI376944	hypothetical protein FLJ11196	Hs.6166	Cluster Incl. AI376944:tc34b06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2066483 /clone_end=3' /gb=AI376944 /gi=4186797 /ug=Hs.6166 /len=492'	0.299454892	3.4283E-07
296	1179	55074_at	W27376	hypothetical protein FLJ10781	Hs.8395	Cluster Incl. W27376:28b7 Homo sapiens cDNA /gb=W27376 /gi=1307036 /ug=Hs.8395 /len=596	0.263536613	1.2408E-05
297	825	44855_s_at	AI971695	hypothetical protein FLJ10659	Hs.107882	Cluster Incl. AI971695:wq88e01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2479128 /clone_end=3' /gb=AI971695 /gi=5768521 /ug=Hs.237607 /len=573'	0.223334551	0.00013093
298	210	44057_at	AA708740	hypothetical protein FLJ10633	Hs.23467	Cluster Incl. AA708740:zl57g12.s1 Homo sapiens cDNA, 3 end /clone=506086 /clone_end=3' /gb=AA708740 /gi=2718658 /ug=Hs.23467 /len=475'	0.142325635	9.6896E-05
299	79	51130_at	AA195220	hypothetical protein FLJ10604	Hs.26516	Cluster Incl. AA195220:zr34g09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-665344 /clone_end=5' /gb=AA195220 /gi=1784932 /ug=Hs.26516 /len=637'	3.915587607	1.4039E-06
300	695	74343_at	AI811688	hypothetical protein FLJ10600	Hs.128766	Cluster Incl. AI811688:tw44g10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2262594 /clone_end=3' /gb=AI811688 /gi=5398254 /ug=Hs.128766 /len=455'	0.33	0.00250076

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
301	313	74690_at	AI016073	hypothetical protein FLJ10578	Hs.131840	Cluster Incl. AI016073:ov26f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1638477 /clone_end=3' /gb=AI016073 /gi=3230409 /ug=Hs.131840 /len=561'	3.07	0.0022939
302	582	58235_at	AI674163	hypothetical protein FLJ10540	Hs.14559	Cluster Incl. AI674163:wc09a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2314652 /clone_end=3' /gb=AI674163 /gi=4874643 /ug=Hs.14559 /len=553'	9.164231149	4.719E-12
303	53	52966_at	AA134589	hypothetical protein FLJ10468	Hs.48855	Cluster Incl. AA134589:zn90b04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-565423 /clone_end=5' /gb=AA134589 /gi=1695586 /ug=Hs.48855 /len=608'	3.058813358	1.3006E-07
304	715	59461_at	AI823992	hypothetical protein FLJ10461	Hs.122579	Cluster Incl. AI823992:wj29c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2404234 /clone_end=3' /gb=AI823992 /gi=5444663 /ug=Hs.122579 /len=564'	4.806177129	9.0609E-08
305	323	54889_at	AI037879	hypothetical protein FLJ10292	Hs.104650	Cluster Incl. AI037879:oy02g12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1664710 /clone_end=3' /gb=AI037879 /gi=3277073 /ug=Hs.104650 /len=654'	3.509937557	1.8056E-05
306	549	64666_at	AI651535	hypothetical protein FLJ10262	Hs.106283	Cluster Incl. AI651535:wb06h08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2304927 /clone_end=3' /gb=AI651535 /gi=4735514 /ug=Hs.43102 /len=587'	0.21534971	7.6457E-06
307	801	52617_at	AI949698	hypothetical protein FLJ10252	Hs.53913	Cluster Incl. AI949698:wq13h04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2471191 /clone_end=3' /gb=AI949698 /gi=5742008 /ug=Hs.42309 /len=553'	3.782457573	0.00028995
308	863	49523_at	AL040063	hypothetical protein FLJ10159	Hs.22505	Cluster Incl. AL040063:DKFZp434P0712_r1 Homo sapiens cDNA, 5 end /clone=DKFZp434P0712 /clone_end=5' /gb=AL040063 /gi=5409033 /ug=Hs.22505 /len=557'	0.18625739	5.3484E-07

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
309	225	48045_at	AA779101	hypothetical protein DKFZp762E1312	Hs.104859	Cluster Incl. AA779101:zj42h12.s1 Homo sapiens cDNA, 3 end /clone=452999 /clone_end=3' /gb=AA779101 /gi=2838432 /ug=Hs.104859 /len=528'	4.802394237	5.8315E-11
310	533	77581_at	AI613455	hypothetical protein DKFZp762D1011	Hs.49933	Cluster Incl. AI613455:ty37b03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2281229 /clone_end=3' /gb=AI613455 /gi=4622622 /ug=Hs.181658 /len=418'	0.27	0.00017758
311	460	87842_at	AI394248	hypothetical protein DKFZp547H236	Hs.284280	Cluster Incl. AI394248:tf78b06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2105363 /clone_end=3' /gb=AI394248 /gi=4223795 /ug=Hs.235588 /len=590'	0.26	0.00279468
312	1245	63581_at	Z78379	hypothetical protein DKFZp434N1928	Hs.279023	Cluster Incl. Z78379:HSZ78379 Homo sapiens cDNA /clone=3.18-(CEPH) /gb=Z78379 /gi=1495152 /ug=Hs.224337 /len=1958	0.262634843	1.5285E-06
313	859	44682_at	AL039400	hypothetical protein DKFZp434K1210	Hs.32352	Cluster Incl. AL039400:DKFZp434K1210_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434K1210 /clone_end=3' /gb=AL039400 /gi=5928554 /ug=Hs.32352 /len=703'	0.269743016	5.019E-05
314	539	53831_at	AI632223	hypothetical protein DKFZp434F2322	Hs.144633	Cluster Incl. AI632223:tt20d07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2241325 /clone_end=3' /gb=AI632223 /gi=4683553 /ug=Hs.144633 /len=721'	0.275006365	5.4416E-07
315	186	72538_at	AA625897	hypothetical protein DKFZp434C0328	Hs.24583	Cluster Incl. AA625897:zu87b02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-744939 /clone_end=3' /gb=AA625897 /gi=2538284 /ug=Hs.222095 /len=252'	0.291337727	0.00026772
316	26	65731_at	AA046671	hyaluronic acid receptor,lymphatic vessel endothelial hyaluronan receptor 1	Hs.278975	Cluster Incl. AA046671:zf12d09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-376721 /clone_end=5' /gb=AA046671 /gi=1524772 /ug=Hs.17917 /len=596'	0.054106026	1.2153E-08

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
317	845	45803_at	AI990409	HSPC150 protein similar to ubiquitin-conjugating enzyme	Hs.5199	Cluster Incl. AI990409:wt74a03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2513164 /clone_end=3' /gb=AI990409 /gi=5837290 /ug=Hs.5199 /len=744'	7.363245733	2.013E-09
318	977	78942_at	F37133	HSPC047 protein	Hs.278943	Cluster Incl. F37133:HSPD35222 Homo sapiens cDNA /clone=sH5-000026-0/F04 /gb=F37133 /gi=4822759 /ug=Hs.185302 /len=337	0.26	0.00165492
319	573	52117_at	AI670876	homeo box C10	Hs.44276	Cluster Incl. AI670876:wa06c12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2297302 /clone_end=3' /gb=AI670876 /gi=4850607 /ug=Hs.44276 /len=798'	3.975570707	0.00126636
320	947	57830_s_at	AW024474	homeo box C10	Hs.44276	Cluster Incl. AW024474:wu76h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990888 /clone_end=3' /gb=AW024474 /gi=5878004 /ug=Hs.236884 /len=229'	3.439858165	0.00508853
321	503	56428_at	AI525822	HN1 protein	Hs.109706	Cluster Incl. AI525822:PT1.3_06_B10.r Homo sapiens cDNA, 5 end /clone_end=5' /gb=AI525822 /gi=4439957 /ug=Hs.109706 /len=773'	5.704063952	6.2245E-06
322	91	39969_at	AA255502	H4 histone family, member G	Hs.46423	Cluster Incl AA255502:zr85b06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-682451 /clone_end=5" /gb=AA255502 /gi=1892406 /ug=Hs.46423 /len=348"	3.965279191	1.93E-08
323	179	90048_at	AA609509	H3 histone, family 3B (H3.3B)	Hs.180877	Cluster Incl. AA609509:af14d11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1031637 /clone_end=3' /gb=AA609509 /gi=2457937 /ug=Hs.238503 /len=381'	0.285742894	2.4107E-05
324	356	88155_at	AI125923	H2B histone family, member B	Hs.180779	Cluster Incl. AI125923:qc41f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1712197 /clone_end=3' /gb=AI125923 /gi=3594437 /ug=Hs.239324 /len=512'	5.05	0.0031179

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
325	756	32609_at	AI885852	H2A histone family, member O	Hs.795	Cluster Incl AI885852:wl62d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2429487 /clone_end=3" /gb=AI885852 /gi=5591016 /ug=Hs.795 /len=580"	3.590913916	1.24E-04
326	40	58445_at	AA115300	guanine nucleotide binding protein (G protein), gamma 2	Hs.23767	Cluster Incl. AA115300:zl09d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-501431 /clone_end=3' /gb=AA115300 /gi=1670497 /ug=Hs.103720 /len=588'	0.226916444	1.5236E-07
327	1163	50271_at	U82984	GTPase activating protein	Hs.23900	Cluster Incl. U82984:U82984 Homo sapiens cDNA /clone=163g24 /gb=U82984 /gi=2731436 /ug=Hs.23900 /len=1771	4.119810176	3.9853E-10
328	969	55630_f_at	D60584	glycogenin 2	Hs.58589	Cluster Incl. D60584:HUM118E12A Homo sapiens cDNA, 3 end /clone=GEN-118E12 /clone_end=3' /gb=D60584 /gi=962223 /ug=Hs.234664 /len=341'	0.172426013	2.305E-06
329	182	91306_s_at	AA613715	gap junction protein, beta 2, 26kD (connexin 26)	Hs.5566	Cluster Incl. AA613715:nq25b01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1144873 /clone_end=3' /gb=AA613715 /gi=2463685 /ug=Hs.81795 /len=607'	12.40	8.5076E-08
330	149	32109_at	AA524547	FXYD domain-containing ion transport regulator 1 (phospholemman)	Hs.160318	Cluster Incl AA524547:ng45h04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-937783 /clone_end=3" /gb=AA524547 /gi=2265475 /ug=Hs.160318 /len=626"	0.259661725	3.05E-08
331	145	54581_at	AA524029	Friedreich ataxia region gene X123	Hs.77889	Cluster Incl. AA524029:ng32f02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-936507 /clone_end=3' /gb=AA524029 /gi=2264957 /ug=Hs.77889 /len=721'	0.233804467	2.6578E-09
332	944	80572_at	AW024276	four and a half LIM domains 1	Hs.239069	Cluster Incl. AW024276:wt69c08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2512718 /clone_end=3' /gb=AW024276 /gi=5877806 /ug=Hs.239069 /len=491'	0.17	1.3623E-06
333	940	45557_r_at	AW021977	fibronectin 1	Hs.118162	Cluster Incl. AW021977:df31c11.y1 Homo sapiens cDNA, 5 end /clone=IMAGE-2484884 /clone_end=5' /gb=AW021977 /gi=5875507 /ug=Hs.237274 /len=320'	5.46370987	1.8509E-07

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
334	70	63893_f_at	AA156998	eukaryotic translation initiation factor 4 gamma, 1	Hs.211568	Cluster Incl. AA156998:zl19e05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-502400 /clone_end=3' /gb=AA156998 /gi=1728613 /ug=Hs.239679 /len=562'	0.097550234	5.0303E-07
335	369	56226_at	AI146465	eukaryotic translation initiation factor 2C, 2	Hs.193053	Cluster Incl. AI146465:qb93c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1707658 /clone_end=3' /gb=AI146465 /gi=3674147 /ug=Hs.193053 /len=633'	3.294370164	2.9946E-05
336	87	75258_f_at	AA224344	ets variant gene 5 (ets-related molecule)	Hs.43697	Cluster Incl. AA224344:zr16d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-663575 /clone_end=3' /gb=AA224344 /gi=1844967 /ug=Hs.237937 /len=420'	0.276576877	0.00020319
337	363	78641_at	AI138998	epidermal growth factor receptor pathway substrate 15	Hs.79095	Cluster Incl. AI138998:qd83f09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1736105 /clone_end=3' /gb=AI138998 /gi=3644970 /ug=Hs.234468 /len=570'	0.31	0.00010017
338	768	59390_at	AI912678	E74-like factor 5 (ets domain transcription factor)	Hs.11713	Cluster Incl. AI912678:we12e04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2340894 /clone_end=3' /gb=AI912678 /gi=5632533 /ug=Hs.11713 /len=587'	0.08111725	6.067E-07
339	166	60058_at	AA557237	DNA segment on chromosome X and Y (unique) 155 expressed sequence	Hs.21595	Cluster Incl. AA557237:nl75d07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1056493 /clone_end=3' /gb=AA557237 /gi=2327714 /ug=Hs.168776 /len=605'	0.311274497	0.00101117
340	937	43506_at	AW020116	DKFZP586P2421 protein	Hs.109439	Cluster Incl. AW020116:df04e10.y1 Homo sapiens cDNA, 5 end /clone=IMAGE-2482675 /clone_end=5' /gb=AW020116 /gi=5873646 /ug=Hs.239240 /len=548'	0.108158864	6.263E-08
341	1197	56409_at	W72194	DKFZP586P1422 protein	Hs.108924	Cluster Incl. W72194:zd69d11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345909 /clone_end=3' /gb=W72194 /gi=1382643 /ug=Hs.108924 /len=631'	0.22460642	7.8076E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
342	1208	44813_s_at	W78050	DKFZP586L2024 protein	Hs.58419	Cluster Incl. W78050:zd78c04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-346758 /clone_end=3' /gb=W78050 /gi=1388613 /ug=Hs.235916 /len=446'	0.185480277	7.5151E-06
343	951	64180_at	AW026659	DKFZP566K1924 protein	Hs.26358	Cluster Incl. AW026659:wv15c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-991047 /clone_end=3' /gb=AW026659 /gi=5880112 /ug=Hs.26358 /len=551'	0.308559272	6.4105E-05
344	839	45501_s_at	AI984087	DKFZP564K1964 protein	Hs.3447	Cluster Incl. AI984087:wz56d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2562063 /clone_end=3' /gb=AI984087 /gi=5811306 /ug=Hs.235102 /len=479'	0.306209896	0.00232454
345	891	39577_at	AL050024	DKFZP564D206 protein	Hs.25956	Cluster Incl AL050024:Homo sapiens mRNA; cDNA DKFZp564D206 (from clone DKFZp564D206) /cds=(0,404) /gb=AL050024 /gi=4884093 /ug=Hs.25956 /len=1409	0.296976926	0.00000163
346	922	60038_at	AW007289	DKFZP434H204 protein	Hs.16441	Cluster Incl. AW007289:wt54f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2511293 /clone_end=3' /gb=AW007289 /gi=5856067 /ug=Hs.16441 /len=552'	3.405694621	6.3581E-06
347	811	48684_at	AI961431	DKFZP434G032 protein	Hs.9029	Cluster Incl. AI961431:wt22e08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2508230 /clone_end=3' /gb=AI961431 /gi=5754144 /ug=Hs.9029 /len=696'	0.222139001	0.00455471
348	886	38057_at	AL049798	dermatopontin	Hs.80552	Cluster Incl AL049798:Human DNA sequence from clone 797M17 on chromosome 1q22-24.3. Contains the DPT gene for Dermatopontin, ESTs, an STS and GSSs /cds=(9,614) /gb=AL049798 /gi=4995638 /ug=Hs.80552 /len=1705	0.215553985	0.000426
349	892	32190_at	AL050118	delta-6 fatty acid desaturase	Hs.184641	Cluster Incl AL050118:Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201) /cds=(0,936) /gb=AL050118 /gi=4884143 /ug=Hs.184641 /len=2621	5.17065685	4.57E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
350	481	74406_at	AI459140	cytochrome c oxidase subunit VIc	Hs.74649	Cluster Incl. AI459140:tj65e06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2146402 /clone_end=3' /gb=AI459140 /gi=4311719 /ug=Hs.129109 /len=499'	0.23	1.3941E-05
351	247	73132_r_at	AA909181	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	Hs.1174	Cluster Incl. AA909181:ol12b04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1523215 /clone_end=3' /gb=AA909181 /gi=3048586 /ug=Hs.234830 /len=526'	4.29	0.00379696
352	1236	90629_at	X84721	cyclin K	Hs.164866	Cluster Incl. X84721:HSEST222 Homo sapiens cDNA /clone=MEC-222 /gb=X84721 /gi=673398 /ug=Hs.164866 /len=558	0.24	0.00136947
353	1100	32242_at	NM_001885	crystallin, alpha B	Hs.1940	Cluster Incl AL038340:DKFZp566K192_s1 Homo sapiens cDNA, 3 end /clone=DKFZp566K192 /clone_end=3" /gb=AL038340 /gi=5407591 /ug=Hs.1940 /len=746"	0.121682021	1.9E-08
354	44	65797_at	AA127736	collagen, type V, alpha 2	Hs.82985	Cluster Incl. AA127736:zk88c12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-489910 /clone_end=5' /gb=AA127736 /gi=1687099 /ug=Hs.237523 /len=616'	3.01095294	0.00679779
355	531	49162_f_at	AI610692	collagen, type I, alpha 2	Hs.179573	Cluster Incl. AI610692:tp40f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2190269 /clone_end=3' /gb=AI610692 /gi=4619859 /ug=Hs.234412 /len=474'	3.125264866	0.00061484
356	457	75384_f_at	AI382415	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	Hs.75106	Cluster Incl. AI382415:ta72b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2049583 /clone_end=3' /gb=AI382415 /gi=4195196 /ug=Hs.239510 /len=418'	0.297772176	5.3744E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
357	457	75382_i_at	AI382415	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	Hs.75106	Cluster Incl. AI382415:ta72b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2049583 /clone_end=3' /gb=AI382415 /gi=4195196 /ug=Hs.239510 /len=418'	0.262336411	2.3579E-06
358	60	64489_at	AA143745	clone HQ0310 PRO0310p1	Hs.279905	Cluster Incl. AA143745:zo31a01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-588456 /clone_end=3' /gb=AA143745 /gi=1713158 /ug=Hs.62273 /len=649'	4.805037919	2.5648E-07
359	889	33611_g_at	AL049977	claudin 8	Hs.162209	Cluster Incl AL049977:Homo sapiens mRNA; cDNA DKFZp564C122 (from clone DKFZp564C122) /cds=UNKNOWN /gb=AL049977 /gi=4884227 /ug=Hs.162209 /len=1071	0.212939754	0.000347
360	158	45574_g_at	AA534688	chromosome 20 open reading frame 1	Hs.9329	Cluster Incl. AA534688:nf75c01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-925728 /clone_end=3' /gb=AA534688 /gi=2278941 /ug=Hs.238349 /len=467'	8.862541971	1.1789E-10
361	882	37630_at	AL049176	chordin-like	Hs.82223	Cluster Incl AL049176:Human DNA sequence from clone 141H5 on chromosome Xq22.1-23. Contains parts of a novel Chordin LIKE protein with von Willebrand factor type C domains. Contains ESTs, STSs and GSSs /cds=(0,767) /gb=AL049176 /gi=4808226 /ug=Hs.82223 /len=3143	0.155185151	0.00000214
362	113	45718_at	AA426499	chondroitin sulfate proteoglycan 2 (versican)	Hs.81800	Cluster Incl. AA426499:zw02b06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-768083 /clone_end=5' /gb=AA426499 /gi=2106744 /ug=Hs.239900 /len=553'	3.067793027	2.8896E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
363	217	75722_at	AA766775	chondroitin 4-sulfotransferase,chondroitin-4-sulfotransferase (C4ST gene)	Hs.240443	Cluster Incl. AA766775:oa35d08.s1 Homo sapiens cDNA /clone=IMAGE-1306959 /gb=AA766775 /gi=2818013 /ug=Hs.163195 /len=440	3.05	7.4702E-06
364	164	50177_at	AA545730	CGI-43 protein	Hs.117582	Cluster Incl. AA545730:HBMSF2G12-REV Homo sapiens cDNA, 5 end /clone=HBMSF2G12 /clone_end=5' /gb=AA545730 /gi=2307100 /ug=Hs.31198 /len=507'	0.174212976	8.7397E-08
365	310	91194_at	AF154332	cell division cycle 2, G1 to S and G2 to M	Hs.184572	Cluster Incl. AF154332:AF154332 Homo sapiens cDNA /clone=CILCA3 /gb=AF154332 /gi=5055942 /ug=Hs.239736 /len=714	5.21	1.4906E-07
366	828	74571_s_at	AI972237	carbonic anhydrase III, muscle specific	Hs.82129	Cluster Incl. AI972237:wr33c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2489474 /clone_end=3' /gb=AI972237 /gi=5769063 /ug=Hs.233663 /len=354'	0.221161273	7.4051E-05
367	586	62987_r_at	AI675178	calcium channel, voltage-dependent, gamma subunit 4	Hs.90207	Cluster Incl. AI675178:tm80g06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2164474 /clone_end=3' /gb=AI675178 /gi=4875658 /ug=Hs.90207 /len=462'	3.355023106	0.03811473
368	275	35717_at	AB020629	ATP-binding cassette, sub-family A (ABC1), member 8	Hs.38095	Cluster Incl AB020629:Homo sapiens mRNA for KIAA0822 protein, complete cds /cds=(138,4883) /gb=AB020629 /gi=4240129 /ug=Hs.38095 /len=5677	0.231001071	1.16E-07
369	547	35390_at	AI651024	ATP-binding cassette, sub-family A (ABC1), member 6	Hs.15780	Cluster Incl AI651024:wa96h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2304059 /clone_end=3" /gb=AI651024 /gi=4735003 /ug=Hs.15780 /len=657"	0.292109229	0.00000833
370	188	64423_s_at	AA628405	ARP1 (actin-related protein 1, yeast) homolog A (centractin alpha)	Hs.153961	Cluster Incl. AA628405:af26b09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1032761 /clone_end=3' /gb=AA628405 /gi=2540792 /ug=Hs.50107 /len=548'	0.23945116	3.194E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
371	685	46108_at	AI804914	ankyrin repeat domain 3	Hs.55565	Cluster Incl. AI804914:tu43d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2253799 /clone_end=3' /gb=AI804914 /gi=5391504 /ug=Hs.55565 /len=535'	0.212140139	3.3556E-06
372	426	46194_at	AI341261	anillin	Hs.62180	Cluster Incl. AI341261:qx85a07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2009268 /clone_end=3' /gb=AI341261 /gi=4078188 /ug=Hs.62180 /len=538'	3.58350616	1.4825E-06
373	392	89031_at	AI218026	amylase, alpha 2A; pancreatic	Hs.203299	Cluster Incl. AI218026:qh21c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1845330 /clone_end=3' /gb=AI218026 /gi=3797841 /ug=Hs.203299 /len=552'	0.263359832	2.0018E-05
374	455	32527_at	AI381790	adipose specific 2	Hs.74120	Cluster Incl AI381790:te41h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2089315 /clone_end=3" /gb=AI381790 /gi=4194571 /ug=Hs.74120 /len=544"	0.215928239	0.000333
375	982	40657_r_at	H15814	adipose most abundant gene transcript 1	Hs.80485	Cluster Incl H15814:yl28b07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-159541 /clone_end=3" /gb=H15814 /gi=880634 /ug=Hs.80485 /len=453"	0.129092155	0.0000909
376	101	58927_at	AA393277	adenylate kinase 5	Hs.18268	Cluster Incl. AA393277:zt74d08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-728079 /clone_end=5' /gb=AA393277 /gi=2046245 /ug=Hs.238152 /len=455'	0.135508105	2.9261E-05
377	965	40155_at	D31883	actin binding LIM protein 1	Hs.158203	Cluster Incl D31883:Human mRNA for KIAA0059 gene, complete cds /cds=(221,1609) /gb=D31883 /gi=505093 /ug=Hs.158203 /len=6754	0.308528713	0.0000126
378	978	80160_at	F37480	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2)	Hs.58324	Cluster Incl. F37480:HSPD36277 Homo sapiens cDNA /clone=sH1-000003-0/G06 /gb=F37480 /gi=4823106 /ug=Hs.221714 /len=408	0.33	0.00059716

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
379	54	64450_at	AA135525	2'-5'oligoadenylate synthetase 3	Hs.56009	Cluster Incl. AA135525:zl09e04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-501438 /clone_end=3' /gb=AA135525 /gi=1696573 /ug=Hs.56009 /len=609'	3.46460752	0.00028766
380	344	58361_at	AI088609		Hs.98558	Cluster Incl. AI088609:qb14e04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1696254 /clone_end=3' /gb=AI088609 /gi=3427668 /ug=Hs.98558 /len=749'	0.14023914	7.756E-06
381	927	75011_at	AW007983		Hs.98518	Cluster Incl. AW007983:wv47f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-991064 /clone_end=3' /gb=AW007983 /gi=5856761 /ug=Hs.236090 /len=211'	0.288607766	0.00049057
382	1184	55720_at	W37770		Hs.9851	Cluster Incl. W37770:zc12g12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-322150 /clone_end=5' /gb=W37770 /gi=1319383 /ug=Hs.9851 /len=573'	0.310758648	1.5774E-06
383	63	49052_at	AA147884		Hs.9812	Cluster Incl. AA147884:zl50b04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-505327 /clone_end=3' /gb=AA147884 /gi=1717300 /ug=Hs.9812 /len=652'	4.823648195	2.3135E-06
384	820	63041_i_at	AI970823		Hs.97876	Cluster Incl. AI970823:wr20c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2488232 /clone_end=3' /gb=AI970823 /gi=5767649 /ug=Hs.97876 /len=452'	0.241006046	3.4955E-06
385	936	45353_s_at	AW016780		Hs.97876	Cluster Incl. AW016780:UI-H-BI0p-abm-f-08-0-UI.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2712350 /clone_end=3' /gb=AW016780 /gi=5865537 /ug=Hs.238149 /len=327'	0.156366951	2.2368E-07
386	792	85521_at	AI935915		Hs.97837	Cluster Incl. AI935915:wo07g11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2454692 /clone_end=3' /gb=AI935915 /gi=5674785 /ug=Hs.188741 /len=405'	6.80	3.8401E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
387	564	51785_s_at	AI659076		Hs.97031	Cluster Incl. AI659076:tt97d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2249487 /clone_end=3' /gb=AI659076 /gi=4762646 /ug=Hs.239118 /len=412'	0.161954139	1.4682E-05
388	577	63035_at	AI672356		Hs.96996	Cluster Incl. AI672356:ty64c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2283842 /clone_end=3' /gb=AI672356 /gi=4852087 /ug=Hs.96996 /len=495'	0.281787455	5.524E-07
389	968	47579_at	D55886		Hs.9572	Cluster Incl. D55886:HUM405B01B Homo sapiens cDNA, 5 end /clone=GEN-405B01 /clone_end=5' /gb=D55886 /gi=970293 /ug=Hs.9572 /len=553'	0.302684307	8.975E-06
390	1112	55484_r_at	R54660		Hs.95511	Cluster Incl. R54660:yj74b11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-154461 /clone_end=3' /gb=R54660 /gi=819118 /ug=Hs.95511 /len=427'	0.12598837	4.8195E-06
391	635	47566_at	AI743671		Hs.94789	Cluster Incl. AI743671:wg41e07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367684 /clone_end=3' /gb=AI743671 /gi=5111959 /ug=Hs.94789 /len=452'	0.248393008	0.00058791
392	93	46737_s_at	AA292431		Hs.92679	Cluster Incl. AA292431:zt28h01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-714481 /clone_end=3' /gb=AA292431 /gi=1940410 /ug=Hs.92679 /len=463'	3.039821602	0.00034656
393	572	55436_at	AI669212		Hs.92127	Cluster Incl. AI669212:wc13c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2315058 /clone_end=3' /gb=AI669212 /gi=4833986 /ug=Hs.92127 /len=596'	3.308493975	0.00068973
394	832	65976_g_at	AI972873		Hs.9167	Cluster Incl. AI972873:wr44f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2490567 /clone_end=3' /gb=AI972873 /gi=5769699 /ug=Hs.9167 /len=594'	0.282705156	2.6139E-08

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
395	832	65975_at	AI972873		Hs.9167	Cluster Incl. AI972873:wr44f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2490567 /clone_end=3' /gb=AI972873 /gi=5769699 /ug=Hs.9167 /len=594'	0.146420991	3.1056E-07
396	629	55610_at	AI742239		Hs.91109	Cluster Incl. AI742239:wg39e09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367496 /clone_end=3' /gb=AI742239 /gi=5110527 /ug=Hs.91109 /len=493'	3.433762656	0.00185863
397	374	77001_at	AI150491		Hs.90756	Cluster Incl. AI150491:qf36b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1752079 /clone_end=3' /gb=AI150491 /gi=3678960 /ug=Hs.126635 /len=485'	0.293369996	0.00208182
398	297	38803_at	AF052142		Hs.90063	Cluster Incl AF052142:Homo sapiens clone 24665 mRNA sequence /cds=UNKNOWN /gb=AF052142 /gi=3360451 /ug=Hs.90063 /len=1486	0.290791559	0.00000576
399	98	52294_s_at	AA351076		Hs.90063	Cluster Incl. AA351076:EST58700 Homo sapiens cDNA, 3 end /clone=ATCC-104314 /clone_end=3' /gb=AA351076 /gi=2003416 /ug=Hs.237155 /len=529'	0.159849377	5.7165E-07
400	894	38786_at	AL079279		Hs.8963	Cluster Incl AL079279:Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 248114 /cds=UNKNOWN /gb=AL079279 /gi=5102585 /ug=Hs.8963 /len=2428	0.316621071	0.00000349
401	919	63994_i_at	AW006898		Hs.88827	Cluster Incl. AW006898:ws15g04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2497302 /clone_end=3' /gb=AW006898 /gi=5855676 /ug=Hs.234094 /len=228'	0.20131865	2.6349E-05
402	132	64813_at	AA481493		Hs.88537	Cluster Incl. AA481493:aa34a10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-815130 /clone_end=3' /gb=AA481493 /gi=2211045 /ug=Hs.88537 /len=406'	0.306142564	0.00010051

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
403	921	47138_at	AW007080		Hs.8817	Cluster Incl. AW007080:ws49h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2500579 /clone_end=3' /gb=AW007080 /gi=5855858 /ug=Hs.8817 /len=523'	0.224326303	1.3801E-05
404	256	62974_at	AA927475		Hs.88162	Cluster Incl. AA927475:om27h03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1542293 /clone_end=3' /gb=AA927475 /gi=3076372 /ug=Hs.88162 /len=536'	0.319186626	6.8126E-06
405	770	48268_at	AI913396		Hs.86619	Cluster Incl. AI913396:wa11g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2297816 /clone_end=3' /gb=AI913396 /gi=5633251 /ug=Hs.86619 /len=503'	4.319893329	1.0223E-07
406	131	62952_at	AA480075		Hs.85015	Cluster Incl. AA480075:zv42b06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-756275 /clone_end=5' /gb=AA480075 /gi=2208226 /ug=Hs.85015 /len=588'	0.300430737	2.2017E-05
407	462	55077_at	AI417267		Hs.84630	Cluster Incl. AI417267:tg76g10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2114754 /clone_end=3' /gb=AI417267 /gi=4260771 /ug=Hs.84630 /len=669'	0.233032608	4.7993E-06
408	415	91320_at	AI288745		Hs.83938	Cluster Incl. AI288745:qm11f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1881549 /clone_end=3' /gb=AI288745 /gi=3932248 /ug=Hs.83938 /len=635'	0.16	2.8399E-09
409	431	62942_at	AI346341		Hs.82669	Cluster Incl. AI346341:qp50b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1926425 /clone_end=3' /gb=AI346341 /gi=4083547 /ug=Hs.82669 /len=549'	0.113945577	5.6167E-06
410	351	54593_at	AI123555		Hs.81796	Cluster Incl. AI123555:qa49h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1690139 /clone_end=3' /gb=AI123555 /gi=3539321 /ug=Hs.81796 /len=585'	0.204459738	1.8002E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
411	1203	54992_at	W73230		Hs.7913	Cluster Incl. W73230:zd56c09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-344656 /clone_end=3' /gb=W73230 /gi=1383364 /ug=Hs.7913 /len=570'	0.29962365	1.8411E-07
412	601	64747_at	AI692878		Hs.76605	Cluster Incl. AI692878:wd42c12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2330806 /clone_end=3' /gb=AI692878 /gi=4970218 /ug=Hs.76605 /len=556'	0.280798539	5.4545E-06
413	27	46274_at	AA046853		Hs.76550	Cluster Incl. AA046853:zf14f11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-376941 /clone_end=5' /gb=AA046853 /gi=1524752 /ug=Hs.76550 /len=669'	3.262260583	2.739E-06
414	853	36894_at	AL031846		Hs.7442	Cluster Incl AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gi=4164368 /ug=Hs.7442 /len=3964	0.27595812	0.00000603
415	304	36119_at	AF070648		Hs.74034	Cluster Incl AF070648:Homo sapiens clone 24651 mRNA sequence /cds=UNKNOWN /gb=AF070648 /gi=3283922 /ug=Hs.74034 /len=1313	0.277326235	0.00000139
416	910	55986_at	AW003215		Hs.73452	Cluster Incl. AW003215:wq64b02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2476011 /clone_end=3' /gb=AW003215 /gi=5850131 /ug=Hs.73452 /len=655'	3.506341539	6.8391E-05
417	1099	57214_at	N95620		Hs.7212	Cluster Incl. N95620:zb66b09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-308537 /clone_end=3' /gb=N95620 /gi=1267890 /ug=Hs.7212 /len=563'	0.29408728	7.2051E-06
418	221	52844_at	AA775711		Hs.72089	Cluster Incl. AA775711:zf31c10.s1 Homo sapiens cDNA, 3 end /clone=378546 /clone_end=3' /gb=AA775711 /gi=2835045 /ug=Hs.72089 /len=513'	0.222082398	5.4948E-09

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
419	56	53762_at	AA142875		Hs.71719	Cluster Incl. AA142875:zl49b06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-505235 /clone_end=3' /gb=AA142875 /gi=1712261 /ug=Hs.71719 /len=450'	0.272334447	0.00059258
420	628	46659_at	AI742057		Hs.7155	Cluster Incl. AI742057:wg38d12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367383 /clone_end=3' /gb=AI742057 /gi=5110345 /ug=Hs.7155 /len=603'	3.317504451	0.00037428
421	1110	64913_at	R51371		Hs.7107	Cluster Incl. R51371:yg76f03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-39107 /clone_end=3' /gb=R51371 /gi=813273 /ug=Hs.7107 /len=542'	0.313288626	5.5293E-06
422	605	46649_at	AI694389		Hs.71058	Cluster Incl. AI694389:wd83b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2338173 /clone_end=3' /gb=AI694389 /gi=4971729 /ug=Hs.71058 /len=514'	0.311833232	2.0222E-07
423	28	65999_at	AA056180		Hs.70704	Cluster Incl. AA056180:zk70f09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-488201 /clone_end=5' /gb=AA056180 /gi=1548518 /ug=Hs.70704 /len=653'	3.820099432	2.0661E-06
424	666	53733_at	AI791751		Hs.68505	Cluster Incl. AI791751:oq53g10.y5 Homo sapiens cDNA, 5 end /clone=IMAGE-1590114 /clone_end=5' /gb=AI791751 /gi=5339562 /ug=Hs.68505 /len=516'	0.307655933	3.7787E-05
425	861	46622_at	AL039870		Hs.6750	Cluster Incl. AL039870:DKFZp434F1012_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434F1012 /clone_end=3' /gb=AL039870 /gi=5408867 /ug=Hs.6750 /len=537'	0.20785966	1.4531E-07
426	799	53724_at	AI948551		Hs.67317	Cluster Incl. AI948551:wp91c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2469132 /clone_end=3' /gb=AI948551 /gi=5740861 /ug=Hs.67317 /len=434'	0.321089692	0.00033754

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
427	893	36821_at	AL050367		Hs.66762	Cluster Incl AL050367:Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026) /cds=UNKNOWN /gb=AL050367 /gi=4914600 /ug=Hs.66762 /len=3938	0.327537441	2.84E-04
428	949	53687_at	AW026241		Hs.65239	Cluster Incl. AW026241:wv10d12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990954 /clone_end=3' /gb=AW026241 /gi=5879771 /ug=Hs.65239 /len=520'	0.215531153	6.5166E-08
429	346	54001_at	AI092936		Hs.6459	Cluster Incl. AI092936:qa81b05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1693137 /clone_end=3' /gb=AI092936 /gi=3431912 /ug=Hs.6459 /len=516'	3.179888739	0.00238804
430	544	46583_at	AI640524		Hs.6382	Cluster Incl. AI640524:wa29b02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2299467 /clone_end=3' /gb=AI640524 /gi=4703633 /ug=Hs.6382 /len=471'	0.262677342	1.7127E-07
431	214	46200_at	AA742697		Hs.62492	Cluster Incl. AA742697:nx30g04.s1 Homo sapiens cDNA /clone=IMAGE-1257654 /gb=AA742697 /gi=2782203 /ug=Hs.62492 /len=526	0.09523078	1.3008E-05
432	1193	62493_at	W68034		Hs.6052	Cluster Incl. W68034:zd39e02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-343034 /clone_end=5' /gb=W68034 /gi=1376903 /ug=Hs.6052 /len=593'	0.311206678	0.00046176
433	212	53200_at	AA723692		Hs.5889	Cluster Incl. AA723692:ah85c11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1325876 /clone_end=3' /gb=AA723692 /gi=2741399 /ug=Hs.5889 /len=491'	0.309546056	0.00039039
434	373	64720_at	AI149693		Hs.58606	Cluster Incl. AI149693:qf42g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1752728 /clone_end=3' /gb=AI149693 /gi=3678162 /ug=Hs.58606 /len=505'	0.305213649	7.743E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
435	1204	46087_at	W73386		Hs.58303	Cluster Incl. W73386:zd53e05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-344384 /clone_end=3' /gb=W73386 /gi=1383519 /ug=Hs.58303 /len=418'	0.241273698	0.00051417
436	22	54407_at	AA044828		Hs.58043	Cluster Incl. AA044828:zk72c09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-488368 /clone_end=3' /gb=AA044828 /gi=1523031 /ug=Hs.58043 /len=641'	0.206509126	4.6226E-06
437	74	62213_at	AA166620		Hs.55778	Cluster Incl. AA166620:zo85f08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-593703 /clone_end=3' /gb=AA166620 /gi=1745209 /ug=Hs.55778 /len=597'	0.168279383	6.2106E-06
438	19	53011_at	AA036952		Hs.50841	Cluster Incl. AA036952:zk30h01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-472081 /clone_end=3' /gb=AA036952 /gi=1510009 /ug=Hs.50841 /len=571'	0.179788238	7.5477E-08
439	678	64694_at	AI799784		Hs.49696	Cluster Incl. AI799784:wc43b08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2321367 /clone_end=3' /gb=AI799784 /gi=5365256 /ug=Hs.49696 /len=382'	0.068952382	1.5685E-09
440	637	52986_at	AI743925		Hs.4944	Cluster Incl. AI743925:wg54f04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2368927 /clone_end=3' /gb=AI743925 /gi=5112213 /ug=Hs.4944 /len=505'	0.28516587	2.5792E-05
441	89	52183_at	AA243659		Hs.4863	Cluster Incl. AA243659:zr68c06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-668554 /clone_end=3' /gb=AA243659 /gi=1874478 /ug=Hs.4863 /len=481'	0.323048827	1.2863E-05
442	37	45786_at	AA082546		Hs.48516	Cluster Incl. AA082546:ze88h10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-366115 /clone_end=5' /gb=AA082546 /gi=1624603 /ug=Hs.48516 /len=567'	0.274783293	4.7788E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
443	383	51012_at	AI200456		Hs.48516	Cluster Incl. AI200456:qf93d03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1757573 /clone_end=3' /gb=AI200456 /gi=3753062 /ug=Hs.235398 /len=347'	0.074704469	2.6745E-08
444	162	64407_at	AA541622		Hs.47447	Cluster Incl. AA541622:ni86c05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-983720 /clone_end=3' /gb=AA541622 /gi=2288056 /ug=Hs.47447 /len=604'	0.237704503	0.00013182
445	876	52140_at	AL046941		Hs.46531	Cluster Incl. AL046941:DKFZp586I0717_r1 Homo sapiens cDNA, 5 end /clone=DKFZp586I0717 /clone_end=5' /gb=AL046941 /gi=5435000 /ug=Hs.46531 /len=704'	0.10436228	5.9049E-07
446	658	62136_at	AI768516		Hs.44038	Cluster Incl. AI768516:wh22g11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2381540 /clone_end=3' /gb=AI768516 /gi=5235025 /ug=Hs.44038 /len=554'	0.279947233	1.5186E-06
447	1065	59014_at	N22378		Hs.43157	Cluster Incl. N22378:yw37d04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-254407 /clone_end=3' /gb=N22378 /gi=1128512 /ug=Hs.43157 /len=450'	0.324029566	4.1704E-06
448	65	45220_at	AA150501		Hs.43148	Cluster Incl. AA150501:zl08g02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-491762 /clone_end=3' /gb=AA150501 /gi=1722015 /ug=Hs.43148 /len=645'	0.276986241	7.1664E-06
449	747	52080_at	AI864898		Hs.43125	Cluster Incl. AI864898:wj66d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2407791 /clone_end=3' /gb=AI864898 /gi=5529005 /ug=Hs.43125 /len=523'	0.07793742	6.2406E-11
450	548	52075_at	AI651212		Hs.4283	Cluster Incl. AI651212:wa98a10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2304186 /clone_end=3' /gb=AI651212 /gi=4735191 /ug=Hs.4283 /len=609'	0.298567674	6.5731E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
451	787	45779_at	AI934361		Hs.42586	Cluster Incl. AI934361:wp04g11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2463908 /clone_end=3' /gb=AI934361 /gi=5673231 /ug=Hs.42586 /len=588'	0.317296872	0.00148036
452	846	45203_at	AI990483		Hs.4243	Cluster Incl. AI990483:ws40b12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2499647 /clone_end=3' /gb=AI990483 /gi=5837364 /ug=Hs.4243 /len=541'	3.149001267	0.00152421
453	512	52019_at	AI557210		Hs.41271	Cluster Incl. AI557210:PT2.1_14_H10.r Homo sapiens cDNA, 3 end /clone_end=3' /gb=AI557210 /gi=4489573 /ug=Hs.41271 /len=867'	8.270850261	1.1279E-08
454	641	85126_at	AI751438		Hs.41271	Cluster Incl. AI751438:cn10a03.y1 Homo sapiens cDNA /clone=NHTBC_cn10a03-(random) /gb=AI751438 /gi=5129702 /ug=Hs.182827 /len=513	3.94	1.5134E-05
455	896	45179_at	AL079707		Hs.41067	Cluster Incl. AL079707:DKFZp434F1430_r1 Homo sapiens cDNA, 5 end /clone=DKFZp434F1430 /clone_end=5' /gb=AL079707 /gi=5435283 /ug=Hs.41067 /len=608'	0.276493253	3.4237E-06
456	1068	46372_at	N25267		Hs.40479	Cluster Incl. N25267:yx74h01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-267505 /clone_end=3' /gb=N25267 /gi=1139417 /ug=Hs.40479 /len=460'	5.223054257	1.848E-05
457	1212	46365_at	W89022		Hs.39421	Cluster Incl. W89022:zh72e09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-417640 /clone_end=3' /gb=W89022 /gi=1403908 /ug=Hs.39421 /len=515'	3.048509737	6.9772E-05
458	254	51970_at	AA921830		Hs.38178	Cluster Incl. AA921830:om44b04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1543855 /clone_end=3' /gb=AA921830 /gi=3069139 /ug=Hs.38178 /len=516'	4.526523002	3.554E-07

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
459	679	65094_at	AI799976		Hs.38163	Cluster Incl. AI799976:wc46f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2321693 /clone_end=3' /gb=AI799976 /gi=5365448 /ug=Hs.38163 /len=540'	0.25714791	2.3349E-06
460	686	49825_at	AI806221		Hs.38022	Cluster Incl. AI806221:wf26e09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2356744 /clone_end=3' /gb=AI806221 /gi=5392787 /ug=Hs.38022 /len=574'	0.279922681	5.5911E-06
461	1170	61727_at	W02608		Hs.36830	Cluster Incl. W02608:za51g08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-296126 /clone_end=5' /gb=W02608 /gi=1274586 /ug=Hs.36830 /len=618'	4.913802444	2.893E-08
462	995	60143_r_at	H71532		Hs.36823	Cluster Incl. H71532:ys11g09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-214528 /clone_end=3' /gb=H71532 /gi=1043348 /ug=Hs.36823 /len=422'	3.065154029	0.01073513
463	485	64252_at	AI479633		Hs.33716	Cluster Incl. AI479633:tm32d12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2158295 /clone_end=3' /gb=AI479633 /gi=4372801 /ug=Hs.33716 /len=488'	0.306446993	0.00164325
464	234	88308_at	AA830307		Hs.32615	Cluster Incl. AA830307:oc49h02.s1 Homo sapiens cDNA /clone=IMAGE-1353075 /gb=AA830307 /gi=2903406 /ug=Hs.32615 /len=416	0.33	1.2131E-05
465	689	45896_at	AI808983		Hs.32458	Cluster Incl. AI808983:wf67d02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2360643 /clone_end=3' /gb=AI808983 /gi=5395549 /ug=Hs.32458 /len=510'	3.165598561	3.3983E-05
466	1206	45757_at	W73855		Hs.32343	Cluster Incl. W73855:zd52f10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-344299 /clone_end=5' /gb=W73855 /gi=1384028 /ug=Hs.32343 /len=677'	0.310421016	0.00080689

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
467	771	44679_at	AI913749		Hs.32241	Cluster Incl. AI913749:wa13d11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2297973 /clone_end=3' /gb=AI913749 /gi=5633604 /ug=Hs.32241 /len=564'	0.286699064	4.1587E-06
468	1173	64238_at	W07043		Hs.32135	Cluster Incl. W07043:za92e08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-300038 /clone_end=5' /gb=W07043 /gi=1281065 /ug=Hs.32135 /len=592'	0.171580051	5.9115E-06
469	865	44575_at	AL040912		Hs.31595	Cluster Incl. AL040912:DKFZp434J0215_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434J0215 /clone_end=3' /gb=AL040912 /gi=5409856 /ug=Hs.31595 /len=665'	0.196081354	1.4632E-05
470	255	61681_at	AA921922		Hs.31412	Cluster Incl. AA921922:om40h06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1543547 /clone_end=3' /gb=AA921922 /gi=3069231 /ug=Hs.31412 /len=488'	0.287881302	0.00063822
471	513	43591_r_at	AI557360		Hs.31297	Cluster Incl. AI557360:PT2.1_6_B08.r Homo sapiens cDNA, 3 end /clone_end=3' /gb=AI557360 /gi=4489723 /ug=Hs.193188 /len=530'	0.324205584	0.00321371
472	636	50955_at	AI743715		Hs.31297	Cluster Incl. AI743715:wg53a08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2368790 /clone_end=3' /gb=AI743715 /gi=5112003 /ug=Hs.37359 /len=489'	0.227579801	0.00228259
473	80	65651_s_at	AA195251		Hs.30835	Cluster Incl. AA195251:zr36d03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-665477 /clone_end=3' /gb=AA195251 /gi=1784951 /ug=Hs.30835 /len=810'	0.309546276	0.00321198
474	347	50658_s_at	AI093702		Hs.30156	Cluster Incl. AI093702:qa31f05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1688385 /clone_end=3' /gb=AI093702 /gi=3432678 /ug=Hs.169169 /len=358'	0.283008853	0.00016645

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
475	33	65626_at	AA059458		Hs.28792	Cluster Incl. AA059458:zl96g05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-512504 /clone_end=5' /gb=AA059458 /gi=1553317 /ug=Hs.28792 /len=572'	13.96572736	5.309E-12
476	687	44025_at	AI806324		Hs.28625	Cluster Incl. AI806324:wf07e07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2349924 /clone_end=3' /gb=AI806324 /gi=5392890 /ug=Hs.28625 /len=559'	0.274066497	7.704E-05
477	474	91773_at	AI439628		Hs.286228	Cluster Incl. AI439628:tc91c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2073516 /clone_end=3' /gb=AI439628 /gi=4305654 /ug=Hs.165670 /len=482'	0.321891202	0.0041327
478	992	78617_at	H54254		Hs.286216	Cluster Incl. H54254:yq89f09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-202985 /clone_end=5' /gb=H54254 /gi=994401 /ug=Hs.227815 /len=492'	0.20	0.00030044
479	206	53490_at	AA705188		Hs.286117	Cluster Incl. AA705188:zj96d09.s1 Homo sapiens cDNA, 3 end /clone=462737 /clone_end=3' /gb=AA705188 /gi=2715106 /ug=Hs.34584 /len=440'	4.243716901	2.469E-12
480	41	52999_at	AA126704		Hs.285995	Cluster Incl. AA126704:zl29b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-503323 /clone_end=3' /gb=AA126704 /gi=1688008 /ug=Hs.50107 /len=588'	0.259103459	0.00021707
481	49	56211_at	AA131648		Hs.285966	Cluster Incl. AA131648:zl33f03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-503741 /clone_end=5' /gb=AA131648 /gi=1693137 /ug=Hs.103720 /len=594'	0.211477764	1.3716E-06
482	588	50408_at	AI680541		Hs.285966	Cluster Incl. AI680541:tw82c09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2266192 /clone_end=3' /gb=AI680541 /gi=4890723 /ug=Hs.25173 /len=1072'	0.131870144	4.6046E-08

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
483	558	88239_i_at	AI656062		Hs.285834	Cluster Incl. AI656062:tt43b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2243503 /clone_end=3' /gb=AI656062 /gi=4740041 /ug=Hs.239724 /len=525'	0.30	0.00017459
484	1171	50990_at	W02823		Hs.285785	Cluster Incl. W02823:za05h04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-291703 /clone_end=5' /gb=W02823 /gi=1274868 /ug=Hs.234963 /len=461'	0.262417057	0.00011017
485	478	59070_at	AI458306		Hs.285590	Cluster Incl. AI458306:tk07c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2150322 /clone_end=3' /gb=AI458306 /gi=4310885 /ug=Hs.184777 /len=585'	3.603536057	0.00024096
486	1175	65988_at	W19285		Hs.285570	Cluster Incl. W19285:zb90g08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-310910 /clone_end=3' /gb=W19285 /gi=1294973 /ug=Hs.202731 /len=460'	0.327647494	0.0008652
487	198	48083_at	AA669106		Hs.285473	Cluster Incl. AA669106:aa81g05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-827384 /clone_end=3' /gb=AA669106 /gi=2630605 /ug=Hs.108106 /len=537'	11.21387388	6.1606E-11
488	838	87998_at	AI983045		Hs.285414	Cluster Incl. AI983045:wz30c01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2559552 /clone_end=3' /gb=AI983045 /gi=5810264 /ug=Hs.237789 /len=566'	0.18	0.00027317
489	815	60842_at	AI963873		Hs.285247	Cluster Incl. AI963873:wt86b08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2514327 /clone_end=3' /gb=AI963873 /gi=5756586 /ug=Hs.227032 /len=704'	0.326231649	5.8287E-05
490	514	78103_at	AI557450		Hs.285233	Cluster Incl. AI557450:PT2.1_7_D12.r Homo sapiens cDNA, 3 end /clone_end=3' /gb=AI557450 /gi=4489813 /ug=Hs.235996 /len=565'	0.22	5.0013E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
491	749	63460_at	AI869951		Hs.285220	Cluster Incl. AI869951:wl63a07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2429556 /clone_end=3' /gb=AI869951 /gi=5543919 /ug=Hs.20854 /len=752'	4.466366979	1.8665E-06
492	1070	83506_at	N31046		Hs.285009	Cluster Incl. N31046:yx51h06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-265307 /clone_end=5' /gb=N31046 /gi=1151445 /ug=Hs.154536 /len=422'	0.31	0.00150517
493	232	51999_at	AA824349		Hs.284269	Cluster Incl. AA824349:aj30f10.s1 Homo sapiens cDNA, 3 end /clone=1391851 /clone_end=3' /gb=AA824349 /gi=2896419 /ug=Hs.40300 /len=888'	0.254762986	8.0203E-05
494	171	48774_at	AA584310		Hs.283713	Cluster Incl. AA584310:nn79g01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1090128 /clone_end=3' /gb=AA584310 /gi=2368919 /ug=Hs.99769 /len=582'	4.911742129	3.4232E-05
495	470	83118_at	AI435443		Hs.276860	Cluster Incl. AI435443:th94e06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2126338 /clone_end=3' /gb=AI435443 /gi=4303218 /ug=Hs.149084 /len=475'	0.27	8.7733E-05
496	59	78658_at	AA143491		Hs.274252	Cluster Incl. AA143491:zo31a09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-588472 /clone_end=5' /gb=AA143491 /gi=1712862 /ug=Hs.239308 /len=552'	0.23	0.00121855
497	379	67167_at	AI188749		Hs.271594	Cluster Incl. AI188749:qd11c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1723400 /clone_end=3' /gb=AI188749 /gi=3739958 /ug=Hs.181742 /len=467'	0.30	2.5913E-05
498	476	84893_at	AI446168		Hs.271530	Cluster Incl. AI446168:tj07h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2140861 /clone_end=3' /gb=AI446168 /gi=4293320 /ug=Hs.176708 /len=435'	4.06	0.00082565

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
499	1103	60202_i_at	R17937		Hs.271363	Cluster Incl. R17937:ye90f06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-125027 /clone_end=3' /gb=R17937 /gi=771547 /ug=Hs.61734 /len=386'	0.315940639	0.00710567
500	199	72092_f_at	AA677864		Hs.271157	Cluster Incl. AA677864:zi13d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-430679 /clone_end=3' /gb=AA677864 /gi=2658386 /ug=Hs.222705 /len=384'	3.07	0.01228173
501	1200	76208_at	W72407		Hs.270549	Cluster Incl. W72407:zd67c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345700 /clone_end=3' /gb=W72407 /gi=1382424 /ug=Hs.118607 /len=651'	0.18	5.7601E-05
502	633	69687_at	AI743516		Hs.270524	Cluster Incl. AI743516:wf72b10.x2 Homo sapiens cDNA, 3 end /clone=IMAGE-2361115 /clone_end=3' /gb=AI743516 /gi=5111804 /ug=Hs.205320 /len=663'	4.593843245	9.3673E-05
503	466	87016_at	AI418596		Hs.270235	Cluster Incl. AI418596:tg37d02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2110947 /clone_end=3' /gb=AI418596 /gi=4264527 /ug=Hs.187926 /len=431'	0.250833383	0.00017276
504	591	91206_at	AI683911		Hs.270027	Cluster Incl. AI683911:tw54f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2263527 /clone_end=3' /gb=AI683911 /gi=4894093 /ug=Hs.145791 /len=497'	0.247069023	0.00654385
505	219	88243_r_at	AA773348		Hs.269628	Cluster Incl. AA773348:ab65g04.s1 Homo sapiens cDNA, 3 end /clone=845718 /clone_end=3' /gb=AA773348 /gi=2824919 /ug=Hs.193254 /len=508'	4.683322065	0.01366367
506	1115	78883_at	R69584		Hs.269392	Cluster Incl. R69584:yi40e04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-141726 /clone_end=3' /gb=R69584 /gi=843101 /ug=Hs.183359 /len=379'	0.28	0.00854584

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
507	1104	49549_at	R20784		Hs.268286	Cluster Incl. R20784:yh18b08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-130071 /clone_end=3' /gb=R20784 /gi=775565 /ug=Hs.227815 /len=452'	0.142950221	9.1918E-06
508	932	80401_at	AW014647		Hs.265499	Cluster Incl. AW014647:UI-H-BI0p-abd-b-12-0-UI.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2711375 /clone_end=3' /gb=AW014647 /gi=5863404 /ug=Hs.234219 /len=402'	0.27	3.1637E-07
509	1111	42913_f_at	R53594		Hs.260164	Cluster Incl. R53594:yj71c01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-154176 /clone_end=3' /gb=R53594 /gi=815496 /ug=Hs.221424 /len=465'	0.092486133	7.5535E-05
510	500	64057_at	AI524085		Hs.25391	Cluster Incl. AI524085:th01e09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2117032 /clone_end=3' /gb=AI524085 /gi=4438220 /ug=Hs.25391 /len=509'	0.194270285	0.00045064
511	566	50411_at	AI659533		Hs.25248	Cluster Incl. AI659533:tu12a12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2250814 /clone_end=3' /gb=AI659533 /gi=4763103 /ug=Hs.25248 /len=654'	0.27933205	6.5167E-06
512	627	61333_at	AI742002		Hs.250879	Cluster Incl. AI742002:wg37f06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367299 /clone_end=3' /gb=AI742002 /gi=5110210 /ug=Hs.239805 /len=490'	3.052533662	0.00715494
513	578	78487_at	AI672389		Hs.250594	Cluster Incl. AI672389:ty64f02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2283867 /clone_end=3' /gb=AI672389 /gi=4852120 /ug=Hs.139891 /len=587'	3.03	0.00127676
514	1114	51886_at	R67627		Hs.24898	Cluster Incl. R67627:yj69c11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-154004 /clone_end=3' /gb=R67627 /gi=840265 /ug=Hs.24898 /len=474'	0.310940166	0.01815078

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
515	24	43919_at	AA045145		Hs.24872	Cluster Incl. AA045145:zf11d12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-376631 /clone_end=5' /gb=AA045145 /gi=1523485 /ug=Hs.24872 /len=588'	0.247364362	0.00047742
516	660	43554_at	AI769199		Hs.24790	Cluster Incl. AI769199:wg35b03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367053 /clone_end=3' /gb=AI769199 /gi=5235708 /ug=Hs.24790 /len=585'	0.280733599	1.293E-05
517	43	50385_at	AA127727		Hs.24715	Cluster Incl. AA127727:zk92d07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-490285 /clone_end=3' /gb=AA127727 /gi=1687016 /ug=Hs.24715 /len=611'	0.324185103	2.1691E-05
518	86	50018_at	AA224205		Hs.24529	Cluster Incl. AA224205:zr15f03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-663485 /clone_end=3' /gb=AA224205 /gi=1844747 /ug=Hs.24529 /len=547'	3.482682058	7.4615E-08
519	522	65523_at	AI583530		Hs.243010	Cluster Incl. AI583530:ts12c08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2228366 /clone_end=3' /gb=AI583530 /gi=4569427 /ug=Hs.192516 /len=490'	0.227760861	1.1547E-07
520	561	50361_at	AI658662		Hs.24192	Cluster Incl. AI658662:tu22a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2251772 /clone_end=3' /gb=AI658662 /gi=4762232 /ug=Hs.24192 /len=503'	0.264360188	3.2473E-05
521	17	60532_at	AA034289		Hs.24192	Cluster Incl. AA034289:zk18e07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-470916 /clone_end=5' /gb=AA034289 /gi=1506098 /ug=Hs.200499 /len=588'	0.221960648	4.0505E-06
522	248	77970_at	AA909818		Hs.241797	Cluster Incl. AA909818:ok81h01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1520401 /clone_end=3' /gb=AA909818 /gi=3050617 /ug=Hs.225822 /len=406'	0.30	0.00326112

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
523	956	50001_at	C16443		Hs.24144	Cluster Incl. C16443:C16443 Homo sapiens cDNA, 5 end /clone=GEN-321F12 /clone_end=5' /gb=C16443 /gi=1571150 /ug=Hs.24144 /len=456'	0.313634138	4.329E-05
524	674	43502_at	AI797276		Hs.23912	Cluster Incl. AI797276:we86f09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2348009 /clone_end=3' /gb=AI797276 /gi=5362748 /ug=Hs.23912 /len=516'	0.232069434	1.5567E-06
525	468	56624_at	AI421837		Hs.23869	Cluster Incl. AI421837:tf55c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2103186 /clone_end=3' /gb=AI421837 /gi=4267768 /ug=Hs.23869 /len=573'	0.31162811	2.5531E-05
526	262	52615_at	AA948319		Hs.237809	Cluster Incl. AA948319:oq46a01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1589352 /clone_end=3' /gb=AA948319 /gi=3109572 /ug=Hs.237809 /len=440'	4.191125642	9.8105E-06
527	1086	56574_at	N57539		Hs.23630	Cluster Incl. N57539:yy81c07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-279948 /clone_end=3' /gb=N57539 /gi=1201429 /ug=Hs.23630 /len=481'	0.325095547	4.0549E-05
528	190	73233_at	AA629715		Hs.235920	Cluster Incl. AA629715:ad43d11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-884469 /clone_end=3' /gb=AA629715 /gi=2552326 /ug=Hs.235920 /len=541'	0.24	1.9829E-05
529	438	66131_at	AI362288		Hs.235758	Cluster Incl. AI362288:qy50h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2015477 /clone_end=3' /gb=AI362288 /gi=4113909 /ug=Hs.235758 /len=416'	3.938205017	0.00035218
530	1178	78622_r_at	W26589		Hs.235390	Cluster Incl. W26589:33d9 Homo sapiens cDNA /gb=W26589 /gi=1307432 /ug=Hs.22954 /len=594	0.20	0.00788877
531	822	43427_at	AI970898		Hs.234898	Cluster Incl. AI970898:wr21c03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2488324 /clone_end=3' /gb=AI970898 /gi=5767724 /ug=Hs.234898 /len=382'	0.290657123	1.7239E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
532	332	49452_at	AI057637		Hs.234898	Cluster Incl. AI057637:oy31h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1667483 /clone_end=3' /gb=AI057637 /gi=3331503 /ug=Hs.21305 /len=599'	0.268475458	1.2854E-06
533	312	55504_at	AI015982		Hs.234545	Cluster Incl. AI015982:ou95e06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1635586 /clone_end=3' /gb=AI015982 /gi=3230318 /ug=Hs.96992 /len=495'	4.250714876	8.7469E-08
534	100	64282_at	AA383718		Hs.234545	Cluster Incl. AA383718:EST97358 Homo sapiens cDNA, 3 end /clone=ATCC-188064 /clone_end=3' /gb=AA383718 /gi=2036227 /ug=Hs.234545 /len=311'	3.197888571	1.2339E-07
535	52	44055_at	AA133979		Hs.23448	Cluster Incl. AA133979:zn88b09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-565241 /clone_end=5' /gb=AA133979 /gi=1691065 /ug=Hs.23448 /len=593'	3.85742898	6.6059E-07
536	821	44974_at	AI970896		Hs.233634	Cluster Incl. AI970896:wr21b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2488317 /clone_end=3' /gb=AI970896 /gi=5767722 /ug=Hs.233634 /len=514'	3.322756779	4.4094E-06
537	834	74340_at	AI978650		Hs.233310	Cluster Incl. AI978650:wr57g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2491838 /clone_end=3' /gb=AI978650 /gi=5803680 /ug=Hs.233310 /len=516'	3.320734927	0.00181461
538	390	74162_r_at	AI208691		Hs.232177	Cluster Incl. AI208691:qg56b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1839151 /clone_end=3' /gb=AI208691 /gi=3770633 /ug=Hs.232177 /len=369'	0.233986843	0.01016812
539	467	43046_at	AI419030		Hs.23202	Cluster Incl. AI419030:tf53b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2102953 /clone_end=3' /gb=AI419030 /gi=4264961 /ug=Hs.23202 /len=473'	0.280053615	2.4083E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
540	1187	57119_s_at	W45581		Hs.23133	Cluster Incl. W45581:zc26c02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-323426 /clone_end=5' /gb=W45581 /gi=1329681 /ug=Hs.23133 /len=587'	0.257584715	7.5905E-05
541	1097	59769_s_at	N91161		Hs.22971	Cluster Incl. N91161:zb12b05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-301809 /clone_end=3' /gb=N91161 /gi=1444488 /ug=Hs.237594 /len=558'	0.174616059	8.6161E-05
542	730	87583_at	AI829520		Hs.227513	Cluster Incl. AI829520:wl19c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2425354 /clone_end=3' /gb=AI829520 /gi=5450191 /ug=Hs.227513 /len=491'	4.00	1.3565E-05
543	809	72501_at	AI956095		Hs.225779	Cluster Incl. AI956095:wt34h04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2509399 /clone_end=3' /gb=AI956095 /gi=5748405 /ug=Hs.225779 /len=502'	0.32	5.2137E-05
544	497	72363_f_at	AI499240		Hs.224902	Cluster Incl. AI499240:to08h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2178483 /clone_end=3' /gb=AI499240 /gi=4391222 /ug=Hs.224902 /len=699'	9.39	0.00152718
545	701	72674_at	AI816835		Hs.222326	Cluster Incl. AI816835:wj34f12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2404751 /clone_end=3' /gb=AI816835 /gi=5435914 /ug=Hs.222326 /len=525'	0.308687757	9.4414E-05
546	123	87339_at	AA451665		Hs.222088	Cluster Incl. AA451665:zx43f11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-789261 /clone_end=5' /gb=AA451665 /gi=2165334 /ug=Hs.222088 /len=464'	3.18	0.00160759
547	425	71899_at	AI339240		Hs.220756	Cluster Incl. AI339240:qt06h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1946845 /clone_end=3' /gb=AI339240 /gi=4076154 /ug=Hs.220756 /len=365'	3.480820479	0.00069879

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
548	90	71839_at	AA251131		Hs.220697	Cluster Incl. AA251131:zs03b12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-684095 /clone_end=3' /gb=AA251131 /gi=1886093 /ug=Hs.220697 /len=365'	3.51886622	0.012637
549	430	42988_at	AI344312		Hs.22011	Cluster Incl. AI344312:tc03e01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2062776 /clone_end=3' /gb=AI344312 /gi=4081518 /ug=Hs.22011 /len=578'	3.531852021	7.7241E-05
550	802	60813_at	AI949833		Hs.21914	Cluster Incl. AI949833:wq14d06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2471243 /clone_end=3' /gb=AI949833 /gi=5742143 /ug=Hs.21914 /len=519'	0.306661245	0.00071317
551	1090	44210_at	N63913		Hs.218707	Cluster Incl. N63913:za27h10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-293827 /clone_end=3' /gb=N63913 /gi=1211742 /ug=Hs.218707 /len=577'	0.085100991	1.0609E-07
552	765	71668_at	AI911149		Hs.218037	Cluster Incl. AI911149:wd24b03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2329037 /clone_end=3' /gb=AI911149 /gi=5630885 /ug=Hs.218037 /len=432'	0.2674744	2.5827E-06
553	532	71524_at	AI610837		Hs.214906	Cluster Incl. AI610837:tp21a12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2188414 /clone_end=3' /gb=AI610837 /gi=4620004 /ug=Hs.214906 /len=571'	0.286772796	3.9564E-05
554	791	91345_at	AI935522		Hs.21415	Cluster Incl. AI935522:wo97e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2463290 /clone_end=3' /gb=AI935522 /gi=5674392 /ug=Hs.9225 /len=845'	0.22	0.00147634
555	774	87161_s_at	AI917447		Hs.213923	Cluster Incl. AI917447:ts84b03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2237933 /clone_end=3' /gb=AI917447 /gi=5637302 /ug=Hs.213923 /len=493'	0.30	0.00020743

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
556	759	71153_i_at	AI888493		Hs.212709	Cluster Incl. AI888493:wn32e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2447162 /clone_end=3' /gb=AI888493 /gi=5593657 /ug=Hs.212709 /len=473'	0.292836533	0.00795029
557	714	87102_at	AI823649		Hs.211535	Cluster Incl. AI823649:wi85g03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2400148 /clone_end=3' /gb=AI823649 /gi=5444320 /ug=Hs.211535 /len=611'	3.74	7.8969E-05
558	717	70733_r_at	AI825341		Hs.211129	Cluster Incl. AI825341:wb17c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2305930 /clone_end=3' /gb=AI825341 /gi=5446012 /ug=Hs.211129 /len=385'	0.302753776	0.03460633
559	842	80045_at	AI989871		Hs.210467	Cluster Incl. AI989871:ws36e12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2499310 /clone_end=3' /gb=AI989871 /gi=5836752 /ug=Hs.210467 /len=722'	3.62	0.00010506
560	680	70350_at	AI800529		Hs.209235	Cluster Incl. AI800529:tc12a08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2063606 /clone_end=3' /gb=AI800529 /gi=5366001 /ug=Hs.209235 /len=439'	3.047280178	0.00648177
561	433	70704_i_at	AI351653		Hs.209078	Cluster Incl. AI351653:qr06h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1940131 /clone_end=3' /gb=AI351653 /gi=4088859 /ug=Hs.209078 /len=400'	0.23	1.3875E-05
562	454	64145_at	AI381686		Hs.208912	Cluster Incl. AI381686:te42a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2089328 /clone_end=3' /gb=AI381686 /gi=4194467 /ug=Hs.239866 /len=278'	6.957639593	1.5821E-06
563	994	70219_at	H68822		Hs.208854	Cluster Incl. H68822:yr77a02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-211274 /clone_end=3' /gb=H68822 /gi=1030250 /ug=Hs.208854 /len=380'	3.289367551	0.00062149

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
564	775	70637_at	AI917901		Hs.208641	Cluster Incl. AI917901:tz14d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2288551 /clone_end=3' /gb=AI917901 /gi=5637756 /ug=Hs.208641 /len=519'	0.20	0.00825561
565	187	70631_at	AA628024		Hs.208558	Cluster Incl. AA628024:nq61f04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1148383 /clone_end=3' /gb=AA628024 /gi=2540023 /ug=Hs.208558 /len=483'	3.01	0.00066989
566	875	70592_at	AL046628		Hs.208207	Cluster Incl. AL046628:DKFZp434N188_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434N188 /clone_end=3' /gb=AL046628 /gi=5434694 /ug=Hs.208207 /len=561'	0.29	3.9E-05
567	567	69893_at	AI659783		Hs.207578	Cluster Incl. AI659783:tt86d01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2248417 /clone_end=3' /gb=AI659783 /gi=4763353 /ug=Hs.207578 /len=452'	0.188450369	5.8656E-06
568	647	86820_at	AI760534		Hs.205696	Cluster Incl. AI760534:wh88b10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2387803 /clone_end=3' /gb=AI760534 /gi=5176201 /ug=Hs.205696 /len=487'	0.31	0.00188255
569	634	89203_at	AI743599		Hs.205690	Cluster Incl. AI743599:wg51e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2368650 /clone_end=3' /gb=AI743599 /gi=5111887 /ug=Hs.205690 /len=570'	3.973692969	7.7231E-05
570	760	86750_at	AI888991		Hs.204044	Cluster Incl. AI888991:wj16b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2402959 /clone_end=3' /gb=AI888991 /gi=5594155 /ug=Hs.204044 /len=528'	0.28	4.6902E-05
571	493	77842_at	AI492879		Hs.203879	Cluster Incl. AI492879:th78b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2124765 /clone_end=3' /gb=AI492879 /gi=4393882 /ug=Hs.203879 /len=521'	12.37	7.3252E-09

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
572	611	75961_at	AI700646		Hs.202259	Cluster Incl. AI700646:we38h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2343421 /clone_end=3' /gb=AI700646 /gi=4988546 /ug=Hs.202259 /len=466'	4.96	7.7642E-05
573	795	86612_at	AI937060		Hs.202040	Cluster Incl. AI937060:wp72f01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2467321 /clone_end=3' /gb=AI937060 /gi=5675930 /ug=Hs.202040 /len=522'	3.17	0.00187143
574	718	69876_at	AI825713		Hs.201875	Cluster Incl. AI825713:wb75g02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2311538 /clone_end=3' /gb=AI825713 /gi=5446384 /ug=Hs.201875 /len=445'	3.64	0.00030428
575	684	69600_at	AI804054		Hs.199996	Cluster Incl. AI804054:tc60g03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2069044 /clone_end=3' /gb=AI804054 /gi=5369526 /ug=Hs.199996 /len=459'	0.29	0.00090022
576	776	79751_at	AI921685		Hs.199713	Cluster Incl. AI921685:wo28g10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2456706 /clone_end=3' /gb=AI921685 /gi=5657649 /ug=Hs.199713 /len=427'	4.11	0.01216522
577	1201	59623_at	W72511		Hs.19827	Cluster Incl. W72511:zd64f08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345447 /clone_end=3' /gb=W72511 /gi=1382168 /ug=Hs.19827 /len=601'	0.263799925	2.9782E-06
578	554	68663_at	AI653487		Hs.197676	Cluster Incl. AI653487:tq94h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2216501 /clone_end=3' /gb=AI653487 /gi=4737466 /ug=Hs.197676 /len=306'	0.300766236	0.00527403
579	813	88622_at	AI962986		Hs.197643	Cluster Incl. AI962986:wt25g06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2508538 /clone_end=3' /gb=AI962986 /gi=5755699 /ug=Hs.197643 /len=391'	0.322154385	0.00084162

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
580	741	69069_at	AI860484		Hs.194274	Cluster Incl. AI860484:wl03b06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2423795 /clone_end=3' /gb=AI860484 /gi=5514100 /ug=Hs.194274 /len=485'	0.26	5.3291E-06
581	817	86154_at	AI968379		Hs.194093	Cluster Incl. AI968379:wu02d12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2515799 /clone_end=3' /gb=AI968379 /gi=5765197 /ug=Hs.194093 /len=577'	0.08	8.2878E-07
582	108	67440_r_at	AA419260		Hs.193745	Cluster Incl. AA419260:zv35c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-755620 /clone_end=3' /gb=AA419260 /gi=2078973 /ug=Hs.185665 /len=456'	4.74	0.00678174
583	651	88814_at	AI761782		Hs.193602	Cluster Incl. AI761782:wi62c08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394830 /clone_end=3' /gb=AI761782 /gi=5177373 /ug=Hs.124852 /len=576'	5.05	1.1628E-06
584	202	88268_at	AA701600		Hs.193491	Cluster Incl. AA701600:zi34h09.s1 Homo sapiens cDNA, 3 end /clone=432737 /clone_end=3' /gb=AA701600 /gi=2704765 /ug=Hs.193491 /len=445'	0.318361618	0.00380632
585	719	85986_at	AI825806		Hs.193142	Cluster Incl. AI825806:td18g01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2076048 /clone_end=3' /gb=AI825806 /gi=5446477 /ug=Hs.193142 /len=707'	0.32	0.00223833
586	211	85943_at	AA719022		Hs.192872	Cluster Incl. AA719022:ah46b08.s1 Homo sapiens cDNA, 3 end /clone=1292535 /clone_end=3' /gb=AA719022 /gi=2732121 /ug=Hs.192872 /len=463'	3.13	5.2381E-08
587	587	68671_at	AI678986		Hs.192671	Cluster Incl. AI678986:tu60e05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2255456 /clone_end=3' /gb=AI678986 /gi=4889168 /ug=Hs.192671 /len=499'	0.19	3.5251E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
588	224	68288_at	AA778816		Hs.192174	Cluster Incl. AA778816:zj38a10.s1 Homo sapiens cDNA, 3 end /clone=452538 /clone_end=3' /gb=AA778816 /gi=2838147 /ug=Hs.192174 /len=505'	0.309129194	0.00126246
589	1102	63131_i_at	R11248		Hs.191935	Cluster Incl. R11248:yf41c02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-129410 /clone_end=5' /gb=R11248 /gi=763983 /ug=Hs.191935 /len=456'	4.256875625	0.00214022
590	260	68047_at	AA936632		Hs.189284	Cluster Incl. AA936632:om58b03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1551341 /clone_end=3' /gb=AA936632 /gi=3094550 /ug=Hs.189284 /len=505'	3.32	0.00044234
591	320	67962_g_at	AI031557		Hs.189040	Cluster Incl. AI031557:ow48d01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1650049 /clone_end=3' /gb=AI031557 /gi=3249769 /ug=Hs.189040 /len=721'	3.428921588	0.00178098
592	598	79037_at	AI692624		Hs.188952	Cluster Incl. AI692624:wd86a10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2338458 /clone_end=3' /gb=AI692624 /gi=4969964 /ug=Hs.188952 /len=569'	3.57	3.57E-05
593	21	46962_at	AA039324		Hs.188861	Cluster Incl. AA039324:zk39d07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-485197 /clone_end=3' /gb=AA039324 /gi=1515602 /ug=Hs.188861 /len=488'	0.212242354	0.00013261
594	410	87087_at	AI283643		Hs.188120	Cluster Incl. AI283643:qj67c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1864532 /clone_end=3' /gb=AI283643 /gi=3921876 /ug=Hs.188120 /len=447'	0.23399829	0.0021469
595	535	67650_at	AI624103		Hs.187319	Cluster Incl. AI624103:ts41h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2231197 /clone_end=3' /gb=AI624103 /gi=4649034 /ug=Hs.187319 /len=432'	0.25	1.0173E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
596	1129	85338_at	T79574		Hs.186579	Cluster Incl. T79574:yd71a01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-113640 /clone_end=3' /gb=T79574 /gi=698083 /ug=Hs.186579 /len=533'	3.57	1.2795E-06
597	110	78954_at	AA420590		Hs.185798	Cluster Incl. AA420590:nc61b10.s1 Homo sapiens cDNA /clone=IMAGE-745723 /gb=AA420590 /gi=2094496 /ug=Hs.185798 /len=501	3.31	0.00081831
598	456	78945_at	AI381930		Hs.185708	Cluster Incl. AI381930:te72f02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2092251 /clone_end=3' /gb=AI381930 /gi=4194711 /ug=Hs.185708 /len=639'	0.21	0.00021905
599	856	92031_g_at	AL037594		Hs.184343	Cluster Incl. AL037594:DKFZp564J0372_s1 Homo sapiens cDNA, 3 end /clone=DKFZp564J0372 /clone_end=3' /gb=AL037594 /gi=5406959 /ug=Hs.239199 /len=795'	3.34	0.02428683
600	239	90745_at	AA846091		Hs.183918	Cluster Incl. AA846091:ak83e05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1414496 /clone_end=3' /gb=AA846091 /gi=2932231 /ug=Hs.183918 /len=464'	3.50	0.00016473
601	1172	67311_at	W05248		Hs.183412	Cluster Incl. W05248:za83a08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-299126 /clone_end=5' /gb=W05248 /gi=1277998 /ug=Hs.183412 /len=473'	3.60	0.00072735
602	553	85168_at	AI653441		Hs.183409	Cluster Incl. AI653441:tq94b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2216441 /clone_end=3' /gb=AI653441 /gi=4737420 /ug=Hs.183409 /len=448'	0.24	1.4344E-05
603	840	89329_at	AI985653		Hs.182809	Cluster Incl. AI985653:wt19b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2507901 /clone_end=3' /gb=AI985653 /gi=5812930 /ug=Hs.182809 /len=765'	0.32	3.5825E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
604	341	91173_at	AI083598		Hs.182364	Cluster Incl. AI083598:ox61c09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1660816 /clone_end=3' /gb=AI083598 /gi=3422021 /ug=Hs.239551 /len=449'	0.22	8.1089E-05
605	873	58999_at	AL044670		Hs.182364	Cluster Incl. AL044670:DKFZp434B1535_r1 Homo sapiens cDNA, 5 end /clone=DKFZp434B1535 /clone_end=5' /gb=AL044670 /gi=5432884 /ug=Hs.182364 /len=495'	0.209357681	6.5741E-07
606	812	61317_f_at	AI962647		Hs.182364	Cluster Incl. AI962647:wq54h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2475123 /clone_end=3' /gb=AI962647 /gi=5755360 /ug=Hs.239551 /len=752'	0.143530024	1.8689E-07
607	3	59812_at	AA004622		Hs.18214	Cluster Incl. AA004622:zh87b06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-428243 /clone_end=3' /gb=AA004622 /gi=1448469 /ug=Hs.18214 /len=509'	3.036525383	0.00011263
608	421	40642_at	AI312646		Hs.181104	Cluster Incl AI312646:qp77f01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1929049 /clone_end=3" /gb=AI312646 /gi=4018251 /ug=Hs.181104 /len=498"	0.268423966	0.0000283
609	92	54826_at	AA284268		Hs.180178	Cluster Incl. AA284268:zc65g03.T7 Homo sapiens cDNA, 3 end /clone=IMAGE-327220 /clone_end=3' /gb=AA284268 /gi=1928550 /ug=Hs.180178 /len=569'	0.309887046	5.8955E-06
610	626	84983_at	AI741880		Hs.179891	Cluster Incl. AI741880:wg48b12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2368319 /clone_end=3' /gb=AI741880 /gi=5110255 /ug=Hs.179891 /len=454'	3.92	3.4377E-07
611	11	63270_at	AA027103		Hs.179673	Cluster Incl. AA027103:zk04e03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-469564 /clone_end=3' /gb=AA027103 /gi=1493312 /ug=Hs.179673 /len=386'	0.214928901	0.00108233

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
612	94	62643_at	AA292789		Hs.179222	Cluster Incl. AA292789:zt56d09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-726353 /clone_end=3' /gb=AA292789 /gi=1941611 /ug=Hs.179222 /len=510'	3.425226104	1.1081E-08
613	1073	78821_at	N39104		Hs.179153	Cluster Incl. N39104:yy45g06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-276538 /clone_end=3' /gb=N39104 /gi=1162311 /ug=Hs.179153 /len=428'	0.32	4.4311E-05
614	389	92131_at	AI206063		Hs.176067	Cluster Incl. AI206063:qg16g01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1759728 /clone_end=3' /gb=AI206063 /gi=3764735 /ug=Hs.176067 /len=504'	4.628098672	0.01037591
615	393	85706_at	AI218358		Hs.175048	Cluster Incl. AI218358:qh21g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1845372 /clone_end=3' /gb=AI218358 /gi=3798173 /ug=Hs.175048 /len=411'	0.325908734	0.00156659
616	391	85702_at	AI215667		Hs.175044	Cluster Incl. AI215667:qm39e01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1884216 /clone_end=3' /gb=AI215667 /gi=3784708 /ug=Hs.175044 /len=461'	3.33211943	0.0264336[illegible]
617	483	85591_at	AI472331		Hs.173975	Cluster Incl. AI472331:tj87d02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2148483 /clone_end=3' /gb=AI472331 /gi=4334421 /ug=Hs.173975 /len=574'	0.268895973	6.8498E-05
618	499	92091_at	AI522299		Hs.173369	Cluster Incl. AI522299:ti76e07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2137956 /clone_end=3' /gb=AI522299 /gi=4436434 /ug=Hs.173369 /len=490'	0.326395709	5.1322E-05
619	4	77540_at	AA007367		Hs.173088	Cluster Incl. AA007367:zh98b03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-429293 /clone_end=3' /gb=AA007367 /gi=1463371 /ug=Hs.173088 /len=462'	4.67	0.00098285

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
620	576	58916_at	AI672101		Hs.17296	Cluster Incl. AI672101:ty63d10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2283763 /clone_end=3' /gb=AI672101 /gi=4851832 /ug=Hs.17296 /len=554'	0.246578758	6.0474E-07
621	479	83000_at	AI458858		Hs.172548	Cluster Incl. AI458858:tj55b07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2145397 /clone_end=3' /gb=AI458858 /gi=4311437 /ug=Hs.172548 /len=485'	3.484499631	0.00090761
622	498	85486_at	AI499334		Hs.171959	Cluster Incl. AI499334:to10d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2178639 /clone_end=3' /gb=AI499334 /gi=4391316 /ug=Hs.171959 /len=462'	0.241109168	0.00358521
623	602	58428_at	AI693178		Hs.171939	Cluster Incl. AI693178:wd68d11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2336757 /clone_end=3' /gb=AI693178 /gi=4970518 /ug=Hs.171939 /len=531'	0.289343463	8.8677E-08
624	325	84627_at	AI039722		Hs.171205	Cluster Incl. AI039722:ox33g02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1658162 /clone_end=3' /gb=AI039722 /gi=3278916 /ug=Hs.171205 /len=488'	0.17	0.00028322
625	508	92007_at	AI540204		Hs.170935	Cluster Incl. AI540204:td10h12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2075303 /clone_end=3' /gb=AI540204 /gi=4457577 /ug=Hs.170935 /len=461'	3.274952213	0.02233069
626	495	85341_at	AI498957		Hs.170861	Cluster Incl. AI498957:tn01c09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2166352 /clone_end=3' /gb=AI498957 /gi=4390939 /ug=Hs.170861 /len=425'	5.310804413	0.00013456
627	130	47972_r_at	AA480009		Hs.169943	Cluster Incl. AA480009:zv18d05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-753993 /clone_end=5' /gb=AA480009 /gi=2208160 /ug=Hs.169943 /len=539'	0.300177072	8.779E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
628	766	62309_at	AI911346		Hs.168941	Cluster Incl. AI911346:wd16a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2328284 /clone_end=3' /gb=AI911346 /gi=5631082 /ug=Hs.168941 /len=396'	0.285068791	0.00347986
629	322	85068_at	AI032972		Hs.167899	Cluster Incl. AI032972:ox22a07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1657044 /clone_end=3' /gb=AI032972 /gi=3253925 /ug=Hs.167899 /len=437'	3.047322219	0.00289855
630	559	58354_at	AI656807		Hs.167771	Cluster Incl. AI656807:tt54b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2244553 /clone_end=3' /gb=AI656807 /gi=4740786 /ug=Hs.167771 /len=531'	3.315735415	3.6415E-07
631	402	84903_f_at	AI264299		Hs.166784	Cluster Incl. AI264299:qk20f06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1869539 /clone_end=3' /gb=AI264299 /gi=3872502 /ug=Hs.166784 /len=396'	0.232010725	1.1163E-05
632	589	84314_at	AI681307		Hs.166674	Cluster Incl. AI681307:tx45g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2272572 /clone_end=3' /gb=AI681307 /gi=4891489 /ug=Hs.166674 /len=551'	0.31	0.00107381
633	112	62277_at	AA424160		Hs.165909	Cluster Incl. AA424160:zv81f03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-760061 /clone_end=3' /gb=AA424160 /gi=2103148 /ug=Hs.165909 /len=447'	5.499256795	3.5001E-06
634	528	82441_f_at	AI590385		Hs.165885	Cluster Incl. AI590385:ts09h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2228115 /clone_end=3' /gb=AI590385 /gi=4599433 /ug=Hs.165885 /len=556'	0.265071246	6.4421E-05
635	871	84763_at	AL044366		Hs.165805	Cluster Incl. AL044366:DKFZp434C022_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434C022 /clone_end=3' /gb=AL044366 /gi=5432588 /ug=Hs.165805 /len=668'	3.725341684	0.00236446

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
636	1062	62707_at	N21031		Hs.164779	Cluster Incl. N21031:yx46f05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-264801 /clone_end=3' /gb=N21031 /gi=1126201 /ug=Hs.164779 /len=554'	0.280524611	2.4112E-05
637	324	62259_at	AI039005		Hs.164680	Cluster Incl. AI039005:ox24g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1657304 /clone_end=3' /gb=AI039005 /gi=3278199 /ug=Hs.164680 /len=483'	0.278599395	0.00054065
638	473	84701_at	AI436670		Hs.164369	Cluster Incl. AI436670:th91b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2125999 /clone_end=3' /gb=AI436670 /gi=4283458 /ug=Hs.164369 /len=393'	3.548116214	1.2564E-07
639	472	75740_at	AI436297		Hs.164226	Cluster Incl. AI436297:th81c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2125074 /clone_end=3' /gb=AI436297 /gi=4309200 /ug=Hs.164226 /len=435'	3.26	7.3767E-05
640	180	84323_at	AA610522		Hs.162697	Cluster Incl. AA610522:np93h10.s1 Homo sapiens cDNA /clone=IMAGE-1133923 /gb=AA610522 /gi=2458950 /ug=Hs.162697 /len=364	5.533470597	0.00288569
641	1078	62701_at	N46855		Hs.16262	Cluster Incl. N46855:yy73e01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-279192 /clone_end=3' /gb=N46855 /gi=1188021 /ug=Hs.16262 /len=524'	0.298063122	0.00073954
642	168	84264_at	AA565654		Hs.162130	Cluster Incl. AA565654:nk25h12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1014599 /clone_end=3' /gb=AA565654 /gi=2337293 /ug=Hs.162130 /len=218'	3.258423603	0.01192547
643	268	81810_at	AA993566		Hs.159983	Cluster Incl. AA993566:ot96g10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1624674 /clone_end=3' /gb=AA993566 /gi=3180111 /ug=Hs.159983 /len=498'	3.012339056	0.00162269

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
644	1127	83908_at	T64637		Hs.159367	Cluster Incl. T64637:yc12h06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-80507 /clone_end=5' /gb=T64637 /gi=673682 /ug=Hs.159367 /len=546'	0.15	2.8623E-06
645	538	91596_at	AI631850		Hs.158992	Cluster Incl. AI631850:wa36h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2300221 /clone_end=3' /gb=AI631850 /gi=4683180 /ug=Hs.158992 /len=491'	3.577532367	0.0140631
646	451	83727_at	AI380583		Hs.158984	Cluster Incl. AI380583:tf95g06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2107066 /clone_end=3' /gb=AI380583 /gi=4190436 /ug=Hs.158984 /len=314'	0.275099238	4.5784E-06
647	783	81659_at	AI928037		Hs.158832	Cluster Incl. AI928037:wo92h01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2462833 /clone_end=3' /gb=AI928037 /gi=5664001 /ug=Hs.158832 /len=583'	0.220904269	2.7534E-07
648	950	81648_at	AW026553		Hs.158741	Cluster Incl. AW026553:wv14h08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990994 /clone_end=3' /gb=AW026553 /gi=5880083 /ug=Hs.158741 /len=522'	0.198202182	0.00027572
649	772	90603_at	AI916544		Hs.158549	Cluster Incl. AI916544:wa26h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2299253 /clone_end=3' /gb=AI916544 /gi=5636399 /ug=Hs.158549 /len=475'	3.99	0.00025369
650	780	81591_r_at	AI924465		Hs.158258	Cluster Incl. AI924465:wn56e01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2449464 /clone_end=3' /gb=AI924465 /gi=5660429 /ug=Hs.158258 /len=384'	0.305190872	0.00039332
651	983	77316_at	H15868		Hs.158113	Cluster Incl. H15868:ym22a12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-48730 /clone_end=5' /gb=H15868 /gi=880688 /ug=Hs.158113 /len=660'	3.01	0.02404954

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
652	440	81459_at	AI367580		Hs.157437	Cluster Incl. AI367580:qv99h11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1989765 /clone_end=3' /gb=AI367580 /gi=4137325 /ug=Hs.157437 /len=348'	0.317481383	0.00152635
653	439	67164_at	AI367020		Hs.157344	Cluster Incl. AI367020:qz23h04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2027767 /clone_end=3' /gb=AI367020 /gi=4136765 /ug=Hs.157344 /len=469'	3.524053838	0.00440287
654	1183	89206_at	W32480		Hs.157099	Cluster Incl. W32480:zc67e03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-327388 /clone_end=5' /gb=W32480 /gi=1313470 /ug=Hs.157099 /len=479'	0.13	9.9516E-05
655	242	81383_at	AA884688		Hs.156974	Cluster Incl. AA884688:am39c01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1471104 /clone_end=3' /gb=AA884688 /gi=2994218 /ug=Hs.156974 /len=409'	4.780974242	0.00216978
656	243	77237_at	AA903473		Hs.153717	Cluster Incl. AA903473:ok58h08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1518207 /clone_end=3' /gb=AA903473 /gi=3038596 /ug=Hs.153717 /len=441'	0.32	0.00692003
657	906	89891_s_at	AW001002		Hs.153385	Cluster Incl. AW001002:wr91d07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2495053 /clone_end=3' /gb=AW001002 /gi=5847918 /ug=Hs.233942 /len=559'	3.120542677	0.00015176
658	1131	61965_at	T83654		Hs.15329	Cluster Incl. T83654:yd67b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-113275 /clone_end=3' /gb=T83654 /gi=711942 /ug=Hs.15329 /len=505'	0.323852128	0.00013054
659	427	83365_at	AI341602		Hs.152932	Cluster Incl. AI341602:qx92g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2010008 /clone_end=3' /gb=AI341602 /gi=4078529 /ug=Hs.152932 /len=461'	3.55	0.03882532

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
660	622	77225_at	AI740516		Hs.152812	Cluster Incl. AI740516:wg16a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2365244 /clone_end=3' /gb=AI740516 /gi=5108804 /ug=Hs.152812 /len=591'	5.38	4.5188E-06
661	177	80845_at	AA603097		Hs.152016	Cluster Incl. AA603097:np37a08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1118486 /clone_end=3' /gb=AA603097 /gi=2436958 /ug=Hs.152016 /len=647'	3.248857169	0.02012519
662	1117	80771_at	R73518		Hs.151079	Cluster Incl. R73518:yj93h12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-156359 /clone_end=3' /gb=R73518 /gi=847550 /ug=Hs.151079 /len=490'	0.237445013	1.6074E-06
663	569	83226_at	AI660245		Hs.150833	Cluster Incl. AI660245:we68h05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2346297 /clone_end=3' /gb=AI660245 /gi=4763815 /ug=Hs.150833 /len=497'	3.60	0.00075917
664	543	80623_s_at	AI640222		Hs.149993	Cluster Incl. AI640222:wa30f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2299613 /clone_end=3' /gb=AI640222 /gi=4703331 /ug=Hs.149993 /len=451'	3.090999056	0.00012996
665	600	91331_at	AI692813		Hs.149425	Cluster Incl. AI692813:wc84d07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2325325 /clone_end=3' /gb=AI692813 /gi=4970153 /ug=Hs.149425 /len=522'	0.139391318	1.5906E-09
666	688	80487_r_at	AI808768		Hs.148867	Cluster Incl. AI808768:wf57h12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2359751 /clone_end=3' /gb=AI808768 /gi=5395334 /ug=Hs.148867 /len=481'	0.296813014	2.4725E-06
667	736	80322_at	AI858012		Hs.147562	Cluster Incl. AI858012:wj69c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2408074 /clone_end=3' /gb=AI858012 /gi=5511628 /ug=Hs.147562 /len=460'	0.323630776	1.7654E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
668	867	83004_r_at	AL042492		Hs.147313	Cluster Incl. AL042492:DKFZp434G1321_r1 Homo sapiens cDNA, 5 end /clone=DKFZp434G1321 /clone_end=5' /gb=AL042492 /gi=5421952 /ug=Hs.147313 /len=668'	0.21	1.1448E-05
669	867	83002_i_at	AL042492		Hs.147313	Cluster Incl. AL042492:DKFZp434G1321_r1 Homo sapiens cDNA, 5 end /clone=DKFZp434G1321 /clone_end=5' /gb=AL042492 /gi=5421952 /ug=Hs.147313 /len=668'	0.07	1.1834E-06
670	366	80209_at	AI140989		Hs.146625	Cluster Incl. AI140989:qf24h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1751003 /clone_end=3' /gb=AI140989 /gi=3648446 /ug=Hs.146625 /len=426'	3.097572971	0.00777918
671	364	61978_at	AI139629		Hs.146562	Cluster Incl. AI139629:qd79g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735742 /clone_end=3' /gb=AI139629 /gi=3645601 /ug=Hs.146562 /len=484'	3.267902315	5.0293E-05
672	408	82941_at	AI277612		Hs.146246	Cluster Incl. AI277612:qm55h08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1892703 /clone_end=3' /gb=AI277612 /gi=3899880 /ug=Hs.146246 /len=459'	0.15	5.9089E-07
673	404	80134_at	AI272054		Hs.146165	Cluster Incl. AI272054:qj89c08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1866638 /clone_end=3' /gb=AI272054 /gi=3891221 /ug=Hs.146165 /len=349'	3.436009136	0.00119052
674	1119	82885_at	R83604		Hs.146059	Cluster Incl. R83604:yp16d05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-187593 /clone_end=5' /gb=R83604 /gi=928481 /ug=Hs.146059 /len=435'	0.24	0.00326683
675	340	82879_at	AI080631		Hs.146042	Cluster Incl. AI080631:ox54b10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1660123 /clone_end=3' /gb=AI080631 /gi=3416882 /ug=Hs.146042 /len=492'	0.29	0.00053988

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
676	918	82860_at	AW006499		Hs.145989	Cluster Incl. AW006499:wt05d12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2506583 /clone_end=3' /gb=AW006499 /gi=5855277 /ug=Hs.145989 /len=513'	0.26	0.00209424
677	712	89087_at	AI821472		Hs.145068	Cluster Incl. AI821472:nj04c07.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-985356 /clone_end=3' /gb=AI821472 /gi=5440551 /ug=Hs.145068 /len=500'	0.15	0.01380957
678	593	77106_at	AI686114		Hs.144871	Cluster Incl. AI686114:tt92c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2248994 /clone_end=3' /gb=AI686114 /gi=4897408 /ug=Hs.144871 /len=495'	0.30	1.7637E-06
679	954	79803_at	AW052142		Hs.144864	Cluster Incl. AW052142:wx26d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2544783 /clone_end=3' /gb=AW052142 /gi=5914501 /ug=Hs.144864 /len=549'	0.309293968	6.6343E-05
680	571	77077_at	AI668620		Hs.144151	Cluster Incl. AI668620:yo53h06.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-181691 /clone_end=3' /gb=AI668620 /gi=4827928 /ug=Hs.144151 /len=617'	0.24	0.04200059
681	519	82595_at	AI570222		Hs.143995	Cluster Incl. AI570222:to76e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2184220 /clone_end=3' /gb=AI570222 /gi=4533596 /ug=Hs.143995 /len=458'	0.23	9.1255E-05
682	623	79618_at	AI740621		Hs.143873	Cluster Incl. AI740621:wg23e12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2365966 /clone_end=3' /gb=AI740621 /gi=5108909 /ug=Hs.143873 /len=457'	0.231031663	0.00044029
683	604	77053_at	AI694059		Hs.143789	Cluster Incl. AI694059:wd67c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2336658 /clone_end=3' /gb=AI694059 /gi=4971399 /ug=Hs.143789 /len=540'	0.28	0.00040144

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
684	193	90421_at	AA633203		Hs.14258	Cluster Incl. AA633203:nq57b02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1147947 /clone_end=3' /gb=AA633203 /gi=2556617 /ug=Hs.14258 /len=570'	6.44	9.8109E-05
685	864	90389_at	AL040178		Hs.142003	Cluster Incl. AL040178:DKFZp434F0213_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434F0213 /clone_end=3' /gb=AL040178 /gi=5409143 /ug=Hs.142003 /len=735'	0.22	4.2869E-07
686	814	69928_at	AI963725		Hs.141024	Cluster Incl. AI963725:wr66b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2492637 /clone_end=3' /gb=AI963725 /gi=5756438 /ug=Hs.207705 /len=427'	3.543032267	0.00038894
687	103	75277_f_at	AA412205		Hs.140996	Cluster Incl. AA412205:zt99g02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-730514 /clone_end=5' /gb=AA412205 /gi=2070972 /ug=Hs.238107 /len=428'	0.326197997	0.00182392
688	1192	91422_at	W63684		Hs.13821	Cluster Incl. W63684:zd30d04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-342151 /clone_end=3' /gb=W63684 /gi=1371265 /ug=Hs.13821 /len=662'	0.29	5.382E-07
689	316	75195_at	AI018237		Hs.137907	Cluster Incl. AI018237:ou19e06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1626754 /clone_end=3' /gb=AI018237 /gi=3232756 /ug=Hs.137907 /len=448'	0.33	0.00918651
690	6	65185_g_at	AA015613		Hs.13766	Cluster Incl. AA015613:ze20f12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-359567 /clone_end=3' /gb=AA015613 /gi=1476661 /ug=Hs.13766 /len=647'	0.29343002	0.0002078
691	507	61191_at	AI539443		Hs.137447	Cluster Incl. AI539443:te51e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2090252 /clone_end=3' /gb=AI539443 /gi=4453578 /ug=Hs.137447 /len=942'	3.063096074	0.00024859

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
692	1080	79133_at	N49591		Hs.137262	Cluster Incl. N49591:yy58d01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-277729 /clone_end=3' /gb=N49591 /gi=1190757 /ug=Hs.137262 /len=459'	0.31404932	1.3855E-05
693	396	82436_at	AI242023		Hs.137003	Cluster Incl. AI242023:qh81a04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1851054 /clone_end=3' /gb=AI242023 /gi=3837420 /ug=Hs.137003 /len=445'	0.25	0.00011435
694	157	82385_at	AA534591		Hs.135657	Cluster Incl. AA534591:nf81b04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-926287 /clone_end=3' /gb=AA534591 /gi=2278844 /ug=Hs.135657 /len=492'	0.24	0.00068507
695	708	78442_at	AI819340		Hs.13561	Cluster Incl. AI819340:wg61a01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2369544 /clone_end=3' /gb=AI819340 /gi=5438419 /ug=Hs.13561 /len=539'	5.00	0.00145442
696	331	78844_at	AI057450		Hs.135405	Cluster Incl. AI057450:ow80c03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1653124 /clone_end=3' /gb=AI057450 /gi=3331316 /ug=Hs.135405 /len=379'	0.127900019	0.00038716
697	979	86587_at	H06350		Hs.135056	Cluster Incl. H06350:yl79g02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-44306 /clone_end=5' /gb=H06350 /gi=869902 /ug=Hs.201607 /len=551'	3.05	0.02123852
698	581	78668_r_at	AI673818		Hs.134665	Cluster Incl. AI673818:to73f12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2183951 /clone_end=3' /gb=AI673818 /gi=4853549 /ug=Hs.134665 /len=201'	4.015935457	0.03600705
699	337	78555_at	AI078121		Hs.134110	Cluster Incl. AI078121:oz24d01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1676257 /clone_end=3' /gb=AI078121 /gi=3412529 /ug=Hs.134110 /len=456'	0.260125725	8.8297E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
700	318	78538_at	AI023295		Hs.134053	Cluster Incl. AI023295:ow95b12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1654559 /clone_end=3' /gb=AI023295 /gi=3239701 /ug=Hs.134053 /len=566'	4.039586551	0.00810637
701	643	76769_at	AI758223		Hs.133471	Cluster Incl. AI758223:ty66b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2284015 /clone_end=3' /gb=AI758223 /gi=5151946 /ug=Hs.133471 /len=535'	0.07	1.664E-06
702	407	90224_at	AI276259		Hs.13337	Cluster Incl. AI276259:ql65f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1877213 /clone_end=3' /gb=AI276259 /gi=3898533 /ug=Hs.13337 /len=505'	3.87	0.00198223
703	329	91875_s_at	AI053741		Hs.133294	Cluster Incl. AI053741:qi69h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1861789 /clone_end=3' /gb=AI053741 /gi=3321528 /ug=Hs.133294 /len=337'	10.36	4.0319E-09
704	596	91873_s_at	AI690773		Hs.133294	Cluster Incl. AI690773:tx99c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2277708 /clone_end=3' /gb=AI690773 /gi=4902075 /ug=Hs.133294 /len=368'	3.15	0.00197051
705	496	78391_at	AI499220		Hs.133226	Cluster Incl. AI499220:to08f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2178461 /clone_end=3' /gb=AI499220 /gi=4391202 /ug=Hs.133226 /len=512'	0.305626072	0.03333431
706	996	65173_at	H92987		Hs.13299	Cluster Incl. H92987:yv07d04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-242023 /clone_end=3' /gb=H92987 /gi=1099315 /ug=Hs.13299 /len=650'	0.280881931	0.00161436
707	321	78231_at	AI031771		Hs.132586	Cluster Incl. AI031771:ow47a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1649948 /clone_end=3' /gb=AI031771 /gi=3249983 /ug=Hs.132586 /len=454'	3.140512538	0.00059354

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
708	763	76703_at	AI890418		Hs.131987	Cluster Incl. AI890418:wm85a12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2442718 /clone_end=3' /gb=AI890418 /gi=5595582 /ug=Hs.131987 /len=516'	0.16	6.3592E-07
709	909	74698_at	AW003102		Hs.131886	Cluster Incl. AW003102:wr03e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2480476 /clone_end=3' /gb=AW003102 /gi=5849940 /ug=Hs.131886 /len=512'	3.09	0.00126632
710	797	77926_at	AI937390		Hs.131170	Cluster Incl. AI937390:wp76f01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2467705 /clone_end=3' /gb=AI937390 /gi=5676260 /ug=Hs.131170 /len=483'	0.271854365	0.00124922
711	537	82120_at	AI631301		Hs.131044	Cluster Incl. AI631301:tz82f05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2295105 /clone_end=3' /gb=AI631301 /gi=4682631 /ug=Hs.131044 /len=462'	0.30	1.7752E-05
712	353	59911_f_at	AI124631		Hs.130893	Cluster Incl. AI124631:am59f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1539879 /clone_end=3' /gb=AI124631 /gi=3593145 /ug=Hs.130893 /len=416'	0.080787812	2.9214E-05
713	693	82094_i_at	AI810266		Hs.130853	Cluster Incl. AI810266:wb86h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2312605 /clone_end=3' /gb=AI810266 /gi=5396832 /ug=Hs.130853 /len=553'	7.28	0.00029449
714	184	47481_at	AA621478		Hs.130699	Cluster Incl. AA621478:af92e12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1055278 /clone_end=3' /gb=AA621478 /gi=2525417 /ug=Hs.130699 /len=398'	0.103783146	4.2586E-09
715	521	90691_at	AI572156		Hs.130316	Cluster Incl. AI572156:te37d05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2088873 /clone_end=3' /gb=AI572156 /gi=4535530 /ug=Hs.130316 /len=344'	3.015818659	0.01303714

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
716	245	77715_at	AA905874		Hs.130123	Cluster Incl. AA905874:oj82c12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1504822 /clone_end=3' /gb=AA905874 /gi=3040997 /ug=Hs.130123 /len=359'	3.808419817	0.00155658
717	709	61908_at	AI820661		Hs.129873	Cluster Incl. AI820661:os32f04.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-1607071 /clone_end=3' /gb=AI820661 /gi=5439740 /ug=Hs.129873 /len=487'	4.615880703	0.00247835
718	491	74462_at	AI492154		Hs.129327	Cluster Incl. AI492154:tg12f12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2108591 /clone_end=3' /gb=AI492154 /gi=4393157 /ug=Hs.129327 /len=547'	0.29	0.00011441
719	739	82009_at	AI859620		Hs.128022	Cluster Incl. AI859620:wm14d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2435919 /clone_end=3' /gb=AI859620 /gi=5513236 /ug=Hs.128022 /len=689'	10.43	7.7763E-10
720	258	91844_at	AA928776		Hs.127630	Cluster Incl. AA928776:on98d10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1564723 /clone_end=3' /gb=AA928776 /gi=3078133 /ug=Hs.127630 /len=503'	0.25	1.9965E-06
721	400	90541_at	AI263819		Hs.127307	Cluster Incl. AI263819:qi09g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1856030 /clone_end=3' /gb=AI263819 /gi=3872022 /ug=Hs.127307 /len=482'	4.421237061	2.399E-05
722	417	77135_at	AI300876		Hs.127229	Cluster Incl. AI300876:qn63e05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1902944 /clone_end=3' /gb=AI300876 /gi=3960222 /ug=Hs.127229 /len=434'	0.054094404	5.2644E-08
723	265	74051_at	AA975530		Hs.126798	Cluster Incl. AA975530:on30g06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1558234 /clone_end=3' /gb=AA975530 /gi=3151322 /ug=Hs.126798 /len=485'	3.09	0.00037957

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
724	526	90069_at	AI589858		Hs.126768	Cluster Incl. AI589858:tm81b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2164509 /clone_end=3' /gb=AI589858 /gi=4598906 /ug=Hs.126768 /len=495'	0.19	1.2217E-06
725	252	46538_at	AA913703		Hs.126733	Cluster Incl. AA913703:ol38e01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1525752 /clone_end=3' /gb=AA913703 /gi=3053095 /ug=Hs.126733 /len=507'	3.31847909	2.3169E-05
726	669	77013_at	AI792817		Hs.126672	Cluster Incl. AI792817:ol64f01.y5 Homo sapiens cDNA, 5 end /clone=IMAGE-1534393 /clone_end=5' /gb=AI792817 /gi=5340533 /ug=Hs.126672 /len=306'	5.050317981	0.00040139
727	244	90479_at	AA905481		Hs.126390	Cluster Incl. AA905481:ok01h09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1506593 /clone_end=3' /gb=AA905481 /gi=3040604 /ug=Hs.126390 /len=461'	3.297301166	7.0947E-06
728	786	73933_at	AI934342		Hs.125780	Cluster Incl. AI934342:wp04e12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2463886 /clone_end=3' /gb=AI934342 /gi=5673212 /ug=Hs.125780 /len=521'	0.26	4.2446E-06
729	172	76770_at	AA584403		Hs.125376	Cluster Incl. AA584403:nn81a05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1090256 /clone_end=3' /gb=AA584403 /gi=2369012 /ug=Hs.125376 /len=512'	0.169055931	4.7816E-06
730	238	73801_at	AA844007		Hs.124436	Cluster Incl. AA844007:ai91d09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1388177 /clone_end=3' /gb=AA844007 /gi=2930458 /ug=Hs.124436 /len=310'	0.25	1.6889E-06
731	240	73794_at	AA848010		Hs.124250	Cluster Incl. AA848010:od24g07.s1 Homo sapiens cDNA /clone=IMAGE-1368924 /gb=AA848010 /gi=2934528 /ug=Hs.124250 /len=415	0.32	4.0015E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
732	477	90009_at	AI458003		Hs.124141	Cluster Incl. AI458003:tj66c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2146476 /clone_end=3' /gb=AI458003 /gi=4312021 /ug=Hs.124141 /len=531'	0.09	4.4423E-07
733	807	59471_at	AI953838		Hs.124015	Cluster Incl. AI953838:wx70b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2548969 /clone_end=3' /gb=AI953838 /gi=5746148 /ug=Hs.124015 /len=640'	5.302996355	1.5522E-06
734	691	57605_at	AI809953		Hs.123933	Cluster Incl. AI809953:wf64b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2360329 /clone_end=3' /gb=AI809953 /gi=5396519 /ug=Hs.123933 /len=615'	0.100992647	4.2459E-08
735	209	65155_at	AA707308		Hs.12369	Cluster Incl. AA707308:zj27a11.s1 Homo sapiens cDNA, 3 end /clone=451484 /clone_end=3' /gb=AA707308 /gi=2717226 /ug=Hs.12369 /len=566'	0.21246828	1.9577E-06
736	858	81670_at	AL037998		Hs.122593	Cluster Incl. AL037998:DKFZp566A091_s1 Homo sapiens cDNA, 3 end /clone=DKFZp566A091 /clone_end=3' /gb=AL037998 /gi=5407308 /ug=Hs.122593 /len=622'	0.17	2.1736E-10
737	16	90316_at	AA033764		Hs.121532	Cluster Incl. AA033764:zk19b11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-470973 /clone_end=5' /gb=AA033764 /gi=1505582 /ug=Hs.121532 /len=446'	3.60100109	0.00094679
738	989	81589_at	H41870		Hs.121518	Cluster Incl. H41870:yo07b09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-177209 /clone_end=5' /gb=H41870 /gi=917922 /ug=Hs.121518 /len=502'	0.24	7.1425E-07
739	409	74760_s_at	AI278074		Hs.120959	Cluster Incl. AI278074:qm57g03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1892884 /clone_end=3' /gb=AI278074 /gi=3900342 /ug=Hs.234191 /len=454'	0.29523189	0.00166257

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
740	387	76326_at	AI201982		Hs.12082	Cluster Incl. AI201982:qs79e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1944314 /clone_end=3' /gb=AI201982 /gi=3754588 /ug=Hs.123318 /len=480'	0.22	3.0941E-06
741	1207	57550_at	W73890		Hs.120785	Cluster Incl. W73890:zd65h02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345555 /clone_end=3' /gb=W73890 /gi=1382285 /ug=Hs.120785 /len=570'	0.285003866	1.5413E-05
742	419	66390_at	AI302387		Hs.120568	Cluster Incl. AI302387:qn50g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1901720 /clone_end=3' /gb=AI302387 /gi=3961733 /ug=Hs.120568 /len=396'	0.239883875	2.9798E-06
743	632	88669_at	AI742521		Hs.120388	Cluster Incl. AI742521:wg43h08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367903 /clone_end=3' /gb=AI742521 /gi=5110809 /ug=Hs.120388 /len=549'	0.24	0.00104631
744	1107	61879_at	R42914		Hs.12024	Cluster Incl. R42914:yg14a10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-32117 /clone_end=3' /gb=R42914 /gi=819821 /ug=Hs.12024 /len=514'	0.198179833	4.3863E-08
745	710	90251_at	AI821005		Hs.118599	Cluster Incl. AI821005:yb59d08.y5 Homo sapiens cDNA, 5 end /clone=IMAGE-75471 /clone_end=5' /gb=AI821005 /gi=5440084 /ug=Hs.118599 /len=507'	3.768700804	0.00159704
746	377	52946_at	AI161367		Hs.118513	Cluster Incl. AI161367:qb80c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1706420 /clone_end=3' /gb=AI161367 /gi=3694611 /ug=Hs.118513 /len=693'	0.204140593	1.3663E-05
747	955	76076_at	AW052186		Hs.118502	Cluster Incl. AW052186:wy87a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2555504 /clone_end=3' /gb=AW052186 /gi=5914545 /ug=Hs.118502 /len=485'	0.240592502	1.5912E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
748	716	57528_at	AI824037		Hs.118392	Cluster Incl. AI824037:wj29h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2404275 /clone_end=3' /gb=AI824037 /gi=5444708 /ug=Hs.118392 /len=603'	0.223181865	3.2934E-06
749	1066	47434_at	N24987		Hs.118338	Cluster Incl. N24987:yx16d11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-261909 /clone_end=5' /gb=N24987 /gi=1139137 /ug=Hs.118338 /len=582'	3.141681584	3.2676E-06
750	609	76029_at	AI698243		Hs.118262	Cluster Incl. AI698243:wa70g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2301560 /clone_end=3' /gb=AI698243 /gi=4986143 /ug=Hs.118262 /len=431'	0.314306045	0.00404612
751	354	76015_at	AI124882		Hs.118121	Cluster Incl. AI124882:am57f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1539687 /clone_end=3' /gb=AI124882 /gi=3593396 /ug=Hs.118121 /len=406'	0.305498776	0.00013207
752	713	57517_at	AI823572		Hs.11782	Cluster Incl. AI823572:wh55g06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2384698 /clone_end=3' /gb=AI823572 /gi=5444243 /ug=Hs.11782 /len=538'	0.325353873	0.00138841
753	655	76163_at	AI766029		Hs.117687	Cluster Incl. AI766029:wh67b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2385775 /clone_end=3' /gb=AI766029 /gi=5232538 /ug=Hs.117687 /len=704'	0.26	0.00090085
754	1108	66305_at	R49146		Hs.117474	Cluster Incl. R49146:yg69h06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-38818 /clone_end=3' /gb=R49146 /gi=820214 /ug=Hs.117474 /len=435'	0.322106515	0.00320729
755	315	66240_s_at	AI016755		Hs.116123	Cluster Incl. AI016755:ov27c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1638538 /clone_end=3' /gb=AI016755 /gi=3231091 /ug=Hs.116123 /len=477'	0.090939502	1.5411E-07

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
756	773	90168_at	AI916626		Hs.116110	Cluster Incl. AI916626:wa28h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2299443 /clone_end=3' /gb=AI916626 /gi=5636481 /ug=Hs.116110 /len=487'	0.139924253	7.063E-09
757	405	88580_at	AI275140		Hs.116104	Cluster Incl. AI275140:ql70h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1877715 /clone_end=3' /gb=AI275140 /gi=3897414 /ug=Hs.116104 /len=444'	8.54	2.0933E-09
758	429	88567_s_at	AI344053		Hs.115838	Cluster Incl. AI344053:tc01h08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2062623 /clone_end=3' /gb=AI344053 /gi=4081259 /ug=Hs.115838 /len=449'	4.52	0.00377036
759	494	76118_at	AI498375		Hs.115497	Cluster Incl. AI498375:tm43e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2160906 /clone_end=3' /gb=AI498375 /gi=4390357 /ug=Hs.115497 /len=487'	0.21	6.3947E-05
760	835	81061_at	AI978710		Hs.115315	Cluster Incl. AI978710:wr58f06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2491907 /clone_end=3' /gb=AI978710 /gi=5803740 /ug=Hs.115315 /len=498'	0.30	5.4104E-05
761	464	89807_at	AI418405		Hs.115173	Cluster Incl. AI418405:tg36e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2110890 /clone_end=3' /gb=AI418405 /gi=4264336 /ug=Hs.115173 /len=472'	0.25	5.4138E-06
762	673	81039_at	AI797063		Hs.114889	Cluster Incl. AI797063:we26e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2342236 /clone_end=3' /gb=AI797063 /gi=5362535 /ug=Hs.114889 /len=506'	0.18	0.00036834
763	1126	54983_at	T64447		Hs.11455	Cluster Incl. T64447:yc10g02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-80306 /clone_end=3' /gb=T64447 /gi=668312 /ug=Hs.11455 /len=563'	0.262512195	0.00069299

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
764	345	75585_at	AI091154		Hs.113750	Cluster Incl. AI091154:oo18a08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1566518 /clone_end=3' /gb=AI091154 /gi=3430213 /ug=Hs.113750 /len=437'	0.093652816	1.6712E-08
765	631	57022_at	AI742490		Hs.112885	Cluster Incl. AI742490:wg43e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367882 /clone_end=3' /gb=AI742490 /gi=5110778 /ug=Hs.112885 /len=550'	0.200282848	5.1114E-07
766	189	80917_at	AA628467		Hs.112572	Cluster Incl. AA628467:af27a01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1032840 /clone_end=3' /gb=AA628467 /gi=2540854 /ug=Hs.112572 /len=520'	0.20	1.9391E-08
767	124	56941_at	AA452295		Hs.110406	Cluster Incl. AA452295:zx30c10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-787986 /clone_end=5' /gb=AA452295 /gi=2165964 /ug=Hs.110406 /len=528'	0.202348411	2.882E-07
768	618	48115_at	AI732274		Hs.11006	Cluster Incl. AI732274:yj68b10.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-153883 /clone_end=3' /gb=AI732274 /gi=5053387 /ug=Hs.11006 /len=538'	0.084843922	6.2396E-05
769	1098	42353_at	N91175		Hs.109653	Cluster Incl. N91175:zb12c10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-301842 /clone_end=3' /gb=N91175 /gi=1444502 /ug=Hs.109653 /len=489'	3.166594901	0.00068815
770	750	56910_at	AI871044		Hs.109525	Cluster Incl. AI871044:wl78h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2431061 /clone_end=3' /gb=AI871044 /gi=5545012 /ug=Hs.109525 /len=486'	0.116868505	2.0122E-05
771	32	63344_at	AA059401		Hs.107253	Cluster Incl. AA059401:zl96c05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-512456 /clone_end=5' /gb=AA059401 /gi=1553304 /ug=Hs.107253 /len=607'	0.269236792	0.00718188

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
772	75	48063_at	AA173572		Hs.10683	Cluster Incl. AA173572:zp04e02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-595418 /clone_end=3' /gb=AA173572 /gi=1753704 /ug=Hs.10683 /len=595'	0.289956429	0.00333978
773	229	58174_at	AA806965		Hs.106771	Cluster Incl. AA806965:oc34c06.s1 Homo sapiens cDNA /clone=IMAGE-1351594 /gb=AA806965 /gi=2876541 /ug=Hs.106771 /len=569	0.212581687	3.0927E-05
774	62	48040_at	AA147751		Hs.103395	Cluster Incl. AA147751:zl50f03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-505373 /clone_end=3' /gb=AA147751 /gi=1717314 /ug=Hs.103395 /len=538'	0.25026049	3.2707E-05
775	753	56190_at	AI885164		Hs.103305	Cluster Incl. AI885164:wl90e04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2432190 /clone_end=3' /gb=AI885164 /gi=5590328 /ug=Hs.103305 /len=506'	3.113529847	2.4582E-06
776	615	58429_at	AI707589		Hs.102793	Cluster Incl. AI707589:as30b05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2318673 /clone_end=3' /gb=AI707589 /gi=4997365 /ug=Hs.102793 /len=461'	0.31991901	0.04026278
777	642	63315_at	AI752682		Hs.102541	Cluster Incl. AI752682:cn18b08.x1 Homo sapiens cDNA /clone=NHTBC_cn18b08-(random) /gb=AI752682 /gi=5130946 /ug=Hs.102541 /len=576	0.194470029	6.4561E-05
778	1199	48032_at	W72347		Hs.102367	Cluster Incl. W72347:zd62c02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345218 /clone_end=3' /gb=W72347 /gi=1382952 /ug=Hs.102367 /len=588'	0.147540619	4.2545E-05
779	386	87970_at	AI201965		Hs.10198	Cluster Incl. AI201965:qs77c03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1944100 /clone_end=3' /gb=AI201965 /gi=3754571 /ug=Hs.237354 /len=392'	0.29	7.7541E-05

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
780	106	63313_at	AA418636		Hs.10198	Cluster Incl. AA418636:zv93e10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-767370 /clone_end=5' /gb=AA418636 /gi=2080455 /ug=Hs.10198 /len=550'	0.244166495	6.125E-07
781	448	64958_at	AI379723		Hs.101689	Cluster Incl. AI379723:tc41b10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2067163 /clone_end=3' /gb=AI379723 /gi=4189576 /ug=Hs.101689 /len=558'	0.275558723	2.9689E-05
782	8	85621_at	AA019424			Cluster Incl. AA019424:ze54d10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-362803 /clone_end=3' /gb=AA019424 /gi=1482062 /ug=Hs.174370 /len=341'	13.54323165	1.6462E-05
783	197	91033_at	AA663786			Cluster Incl. AA663786:ae72f07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-969733 /clone_end=3' /gb=AA663786 /gi=2617777 /ug=Hs.231804 /len=395'	8.54	0.00415608
784	263	83836_at	AA968657			Cluster Incl. AA968657:oq76c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1592260 /clone_end=3' /gb=AA968657 /gi=3143837 /ug=Hs.159927 /len=524'	8.025997484	0.00016062
785	728	73388_at	AI829169			Cluster Incl. AI829169:wk76b02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2421291 /clone_end=3' /gb=AI829169 /gi=5449840 /ug=Hs.226392 /len=456'	5.726391287	4.0981E-05
786	201	87667_at	AA701188			Cluster Incl. AA701188:zj80a04.s1 Homo sapiens cDNA, 3 end /clone=461166 /clone_end=3' /gb=AA701188 /gi=2704353 /ug=Hs.190357 /len=310'	3.734521363	0.00451133
787	970	82685_at	D63177			Cluster Incl. D63177:HUM501F10B Homo sapiens cDNA, 5 end /clone=GEN-501F10 /clone_end=5' /gb=D63177 /gi=966846 /ug=Hs.167615 /len=441'	3.65368217	0.00170328

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
788	319	66998_at	AI025199			Cluster Incl. AI025199:ov40f01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1639801 /clone_end=3' /gb=AI025199 /gi=3240812 /ug=Hs.131604 /len=427'	3.149965078	8.1229E-05
789	36	79496_r_at	AA081045			Cluster Incl. AA081045:zn33e02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-549242 /clone_end=3' /gb=AA081045 /gi=1623033 /ug=Hs.193281 /len=522'	0.32	0.00070373
790	1186	47889_at	W44656			Cluster Incl. W44656:zc29a09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-323704 /clone_end=5' /gb=W44656 /gi=1330176 /ug=Hs.14627 /len=599'	0.317111476	9.1295E-07
791	869	65867_at	AL043089			Cluster Incl. AL043089:DKFZp434C1123_r1 Homo sapiens cDNA, 5 end /clone=DKFZp434C1123 /clone_end=5' /gb=AL043089 /gi=5422506 /ug=Hs.3807 /len=762'	0.297990459	1.7708E-06
792	1190	57586_at	W56090			Cluster Incl. W56090:zc56g03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-326356 /clone_end=5' /gb=W56090 /gi=1357999 /ug=Hs.12319 /len=620'	0.264521584	3.3328E-06
793	5	82582_at	AA007390			Cluster Incl. AA007390:zh99a06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-429394 /clone_end=5' /gb=AA007390 /gi=1463628 /ug=Hs.166944 /len=555'	0.233645562	7.1154E-05
794	117	48927_at	AA430314			Cluster Incl. AA430314:zw68h06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-781403 /clone_end=5' /gb=AA430314 /gi=2113524 /ug=Hs.95296 /len=579'	0.185193232	1.3678E-06
795	1174	53793_at	W07304			Cluster Incl. W07304:za97b10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-300475 /clone_end=5' /gb=W07304 /gi=1281502 /ug=Hs.12927 /len=578'	0.182339389	5.8223E-06

#	SeqID	Affy	Genbank	Gene Name	Cluster #	Cluster Description	Fold Change	p-values
796	1081	84535_at	N50065			Cluster Incl. N50065:yz10h03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-282677 /clone_end=3' /gb=N50065 /gi=1191231 /ug=Hs.169732 /len=550'	0.14	6.1089E-05
797	1116	52449_at	R70255			Cluster Incl. R70255:yj81f06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-155171 /clone_end=3' /gb=R70255 /gi=843772 /ug=Hs.25150 /len=367'	0.110161171	2.7057E-06

Table 3: 35 Genes from HCA cluster node 2761X

#	SeqID	Affy	Genbank	Gene Name	Fold Change	Fold Change (ratio)	p-value
1	127	39271_at	AA461365	melanoma inhibitory activity,ras-related GTP-binding protein 4b	-4.06	0.246437105	5.020000E-05
2	959	1197_at	D00654	actin, gamma 2, smooth muscle, enteric	-11.01	0.090848213	3.510000E-07
3	964	34203_at	D17408	calponin 1, basic, smooth muscle	-10.98	0.091111614	2.660000E-08
4	288	37407_s_at	AF013570	myosin, heavy polypeptide 11, smooth muscle	-10.77	0.092826583	2.360000E-05
5	453	58774_at	AI380979	eukaryotic translation initiation factor 4 gamma, 1	-9.02	0.110855696	7.124464E-06
6	283	767_at	AF001548	myosin, heavy polypeptide 11, smooth muscle	-8.20	0.121953593	1.340000E-05
7	70	63893_f_at	AA156998	eukaryotic translation initiation factor 4 gamma, 1	-5.94	0.168279383	6.210594E-06
8	1023	37909_at	L34155	laminin, alpha 3 (nicein (150kD), kalinin (165kD), BM600 (150kD), epilegrin)	-5.33	0.187743879	4.710000E-08
9	1223	37765_at	X54162	leiomodin 1 (smooth muscle)	-4.58	0.218509986	1.380000E-06
10	17	60532_at	AA034289		-4.51	0.221960648	4.050474E-06
11	1197	56409_at	W72194	DKFZP586P1422 protein	-4.45	0.22460642	7.807645E-06
12	960	773_at	D10667		-4.37	0.228917694	4.150000E-04
13	162	64407_at	AA541622		-4.21	0.237704503	1.318202E-04
14	1141	36929_at	U17760	laminin, beta 3 (nicein (125kD), kalinin (140kD), BM600 (125kD))	-3.85	0.260055335	4.120000E-07
15	561	50361_at	AI658662		-3.78	0.264360188	3.247311E-05
16	1151	32847_at	U48959	myosin, light polypeptide kinase	-3.58	0.279338963	1.610000E-04
17	658	62136_at	AI768516		-3.57	0.279947233	1.518608E-06
18	1013	41524_at	L08488	inositol polyphosphate-1-phosphatase	-3.56	0.281207961	3.900000E-07
19	832	65975_at	AI972873		-3.54	0.282705156	2.613853E-08
20	1099	57214_at	N95620		-3.40	0.29408728	7.205058E-06
21	869	65867_at	AL043089		-3.36	0.297990459	1.770803E-06
22	956	50001_at	C16443		-3.19	0.313634138	4.329042E-05
23	973	38048_at	D84110	RNA-binding protein gene with multiple splicing	-3.09	0.323566748	1.000000E-04
24	150	46276_at	AA526844	myosin, light polypeptide kinase	-3.06	0.32670528	4.436191E-07
25	272	41137_at	AB007972		-2.72	0.36717276	2.373819E-06
26	289	34797_at	AF014402	phosphatidic acid phosphatase type 2A	-2.41	0.415471413	1.093627E-04
27	974	34162_at	D84111	RNA-binding protein gene with multiple splicing	-2.45	0.407999585	1.086072E-05

#	SeqID	Affy	Genbank	Gene Name	Fold Change	Fold Change (ratio)	p-value
28	237	66529_at	AA843926		-2.57	0.389097343	2.789025E-04
29	449	49540_at	AI379892		-2.62	0.381989673	5.432773E-06
30	520	49300_at	AI571525		-2.11	0.473538178	1.694770E-05
31	638	65734_at	AI744109		-2.13	0.47055836	3.251490E-06
32	767	46653_at	AI912571	CGI-43 protein	-2.18	0.458611832	1.715459E-03
33	1202	49349_at	W72919	DKFZP564B0769 protein	-2.87	0.348051542	4.653880E-06
34	1210	47076_at	W87690		-2.72	0.367062886	4.038920E-05
35	1211	54668_at	W88427		-2.46	0.406092748	3.551680E-04

Table 4: BREAST / INFILTRATING DUCT CARCINOMA

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
1	1	AA001250	X	X	X	X	340.76+/-99.54 175.47+/-67.36 N1=40, N2=10 Fold Change: 2.01 P-value: .00096
2	7	AA017070	218.33+/-195.52 75.87+/-104.51 N1=40, N2=168 Fold Change: 2.8 P-value: 0	X	X	218.33+/-195.52 49.83+/-71.53 N1=40, N2=31 Fold Change: 3.67 P-value: 0	218.33+/-195.52 28.53+/-33.27 N1=40, N2=10 Fold Change: 5.14 P-value: 0
3	11	AA027103	252.16+/-278.17 53.89+/-220.22 N1=39, N2=168 Fold Change: 3.64 P-value: 0	X	252.16+/-278.17 47.94+/-61.86 N1=39, N2=10 Fold Change: 3.3 P-value: .01164	252.16+/-278.17 14.48+/-36.79 N1=39, N2=31 Fold Change: 4.51 P-value: 0	252.16+/-278.17 15.58+/-46.81 N1=39, N2=6 Fold Change: 4.88 P-value: 0
4	12	AA029437	221.16+/-280.96 57.63+/-138.17 N1=40, N2=168 Fold Change: 3.25 P-value: 0	X	X	221.4+/-284.63 86.7+/-207.7 N1=40, N2=31 Fold Change: 2.95 P-value: .00006	X
5	13	AA029735	X	X	X	X	581.98+/-218.36 246.82+/-189 N1=40, N2=10 Fold Change: 2.76 P-value: .00174
6	15	AA031790	X	X	X	X	336.45+/-181.35 122.36+/-61.84 N1=40, N2=10 Fold Change: 2.82 P-value: .0009
7	17	AA034289	203.74+/-150.5 30.48+/-63.02 N1=39, N2=168 Fold Change: 4.19 P-value: 0	X	203.74+/-150.5 56.05+/-43.37 N1=39, N2=10 Fold Change: 2.69 P-value: .00466	203.74+/-150.5 41.75+/-90.59 N1=39, N2=31 Fold Change: 3.95 P-value: 0	203.74+/-150.5 -7.27+/-28.68 N1=39, N2=6 Fold Change: 6.91 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
8	18	AA034418	370.77+/-175.09 171.84+/-132.49 N1=40, N2=168 Fold Change: 2.41 P-value: 0	X	X	367.92+/-176.43 145.41+/-92.73 N1=40, N2=31 Fold Change: 2.76 P-value: 0	367.92+/-176.43 148.75+/-103.92 N1=40, N2=10 Fold Change: 2.55 P-value: .00125
9	20	AA037766	X	X	X	217.99+/-102.27 98.41+/-70 N1=39, N2=31 Fold Change: 2.21 P-value: 0	X
10	22	AA044828	228.22+/-120.36 81.18+/-75.97 N1=40, N2=168 Fold Change: 2.87 P-value: 0	X	X	228.25+/-121.93 68.84+/-62.87 N1=40, N2=31 Fold Change: 3.18 P-value: 0	228.25+/-121.93 30.55+/-34.05 N1=40, N2=10 Fold Change: 5.8 P-value: 0
11	23	AA044830	384.63+/-189.59 195.74+/-112.66 N1=40, N2=168 Fold Change: 2.09 P-value: 0	X	X	387.92+/-190.91 142.87+/-73.75 N1=40, N2=31 Fold Change: 2.81 P-value: 0	387.92+/-190.91 148.94+/-75.02 N1=40, N2=10 Fold Change: 2.65 P-value: .00182
12	24	AA045145	261.46+/-178.02 83.44+/-183.41 N1=40, N2=168 Fold Change: 3.35 P-value: 0	X	X	262.21+/-180.28 63.71+/-149.37 N1=40, N2=31 Fold Change: 4 P-value: 0	262.21+/-180.28 8.27+/-106.8 N1=40, N2=10 Fold Change: 5.08 P-value: .00018
13	25	AA046457	X	X	254.96+/-154.86 91.58+/-30.86 N1=40, N2=6 Fold Change: 2.4 P-value: .00032	X	254.96+/-154.86 99.01+/-89.62 N1=40, N2=10 Fold Change: 2.75 P-value: .00204
14	27	AA046853	200.27+/-196.52 385.33+/-229.71 N1=40, N2=168 Fold Change: 2.07 P-value: 0	X	201.69+/-198.89 406.89+/-152.52 N1=40, N2=6 Fold Change: 2.42 P-value: .0008	201.69+/-198.89 428.46+/-216.88 N1=40, N2=31 Fold Change: 2.44 P-value: 0	201.69+/-198.89 370.09+/-174.14 N1=40, N2=10 Fold Change: 2.06 P-value: .00306

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
15	28	AA056180	X	X	X	X	80.83+/-48.85 254.08+/-148.48 N1=40, N2=10 Fold Change: 3.07 P-value: .00013
16	29	AA056755	X	X	243+/-190.55 413.4+/-148.7 N1=40, N2=6 Fold Change: 2.12 P-value: .00235	243+/-190.55 476.92+/-268.57 N1=40, N2=31 Fold Change: 2.22 P-value: .00002	X
17	30	AA058578	X	X	X	282.9+/-254.52 100.56+/-94.65 N1=40, N2=31 Fold Change: 2.24 P-value: .00272	282.9+/-254.52 62.96+/-63.59 N1=40, N2=10 Fold Change: 3.01 P-value: .00335
18	31	AA059396	383.9+/-126.38 184.18+/-88.67 N1=40, N2=168 Fold Change: 2.2 P-value: 0	X	X	383.25+/-127.97 195.3+/-91.8 N1=40, N2=31 Fold Change: 2.03 P-value: 0	383.25+/-127.97 164.81+/-71.68 N1=40, N2=10 Fold Change: 2.37 P-value: .00006
19	32	AA059401	444.15+/-409.74 108.09+/-137.58 N1=40, N2=168 Fold Change: 3.84 P-value: 0	X	450.12+/-413.33 84.82+/-108.93 N1=40, N2=6 Fold Change: 4.32 P-value: .01621	450.12+/-413.33 78.85+/-105.76 N1=40, N2=31 Fold Change: 5.13 P-value: 0	450.12+/-413.33 4.41+/-98.3 N1=40, N2=10 Fold Change: 7.56 P-value: 0
20	33	AA059458	73.64+/-89.7 421.17+/-253.37 N1=40, N2=168 Fold Change: 6.85 P-value: 0	X	74.76+/-90.6 328.32+/-224.02 N1=40, N2=6 Fold Change: 4.88 P-value: .00774	74.76+/-90.6 373.99+/-269.57 N1=40, N2=31 Fold Change: 5.56 P-value: 0	74.76+/-90.6 399.15+/-254.81 N1=40, N2=10 Fold Change: 5.85 P-value: .00035
21	34	AA075632	X	X	X	331.71+/-236.88 176.14+/-256.71 N1=40, N2=31 Fold Change: 2.48 P-value: .0012	331.71+/-236.88 125.73+/-212.88 N1=40, N2=10 Fold Change: 4.1 P-value: .00867

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
22	35	AA079839	X	X	X	399.21+/-217.44 178.24+/-173.52 N1=39, N2=31 Fold Change: 2.2 P-value: .00001	399.21+/-217.44 173.1+/-209.18 N1=39, N2=6 Fold Change: 2.61 P-value: .00239
23	37	AA082546	272.4+/-223.42 105.34+/-63.79 N1=40, N2=168 Fold Change: 2.35 P-value: 0	X	X	275.39+/-225.53 93.91+/-47.44 N1=40, N2=31 Fold Change: 2.55 P-value: 0	275.39+/-225.53 74.83+/-36.32 N1=40, N2=10 Fold Change: 3.23 P-value: .00005
24	38	AA101125	X	X	X	670.66+/-337.66 325+/-154.53 N1=40, N2=31 Fold Change: 2.01 P-value: 0	670.66+/-337.66 292.03+/-126.99 N1=40, N2=10 Fold Change: 2.27 P-value: .00091
25	41	AA126704	314.32+/-135.99 107.92+/-81.49 N1=40, N2=168 Fold Change: 3.17 P-value: 0	X	X	312.64+/-137.34 77.02+/-71.72 N1=40, N2=31 Fold Change: 4.14 P-value: 0	312.64+/-137.34 78.95+/-75.5 N1=40, N2=10 Fold Change: 3.75 P-value: .00032
26	42	AA127718	238.22+/-357.2 82.46+/-76.05 N1=40, N2=168 Fold Change: 2.53 P-value: 0	X	X	240.21+/-361.64 87.69+/-80.58 N1=40, N2=31 Fold Change: 2.39 P-value: .00006	X
27	43	AA127727	214.24+/-122.15 81.63+/-51.81 N1=40, N2=168 Fold Change: 2.72 P-value: 0	X	212.97+/-123.48 89.92+/-52.2 N1=40, N2=6 Fold Change: 2.29 P-value: .00795	212.97+/-123.48 66.11+/-40.88 N1=40, N2=31 Fold Change: 3.29 P-value: 0	212.97+/-123.48 51.85+/-29.44 N1=40, N2=10 Fold Change: 3.99 P-value: .00001
28	47	AA131456	642.53+/-392.68 325.78+/-211.65 N1=40, N2=168 Fold Change: 2.13 P-value: 0	X	X	650.36+/-394.64 340.69+/-188.84 N1=40, N2=31 Fold Change: 2.01 P-value: 0	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
29	48	AA131632	X	X	X	376.43+/-162.83 185.82+/-88.41 N1=40, N2=31 Fold Change: 2.11 P-value: 0	X
30	50	AA131894	X	X	X	X	125.64+/-46.19 310.35+/-183.98 N1=40, N2=10 Fold Change: 2.19 P-value: .00585
31	51	AA133248	401.89+/-133.14 193.81+/-109.33 N1=40, N2=168 Fold Change: 2.26 P-value: 0	X	X	X	400.91+/-134.73 182.12+/-50.15 N1=40, N2=10 Fold Change: 2.15 P-value: 0
32	55	AA137038	X	X	X	122.53+/-86.86 266.01+/-205.87 N1=40, N2=31 Fold Change: 2.11 P-value: .00008	X
33	57	AA142913	302.75+/-219.97 88.13+/-60.53 N1=40, N2=168 Fold Change: 3.49 P-value: 0	X	302.34+/-222.83 104.62+/-49.26 N1=40, N2=6 Fold Change: 2.6 P-value: .00174	302.34+/-222.83 84.31+/-62.54 N1=40, N2=31 Fold Change: 3.74 P-value: 0	302.34+/-222.83 83.75+/-83.82 N1=40, N2=10 Fold Change: 4.01 P-value: .00014
34	59	AA143491	491.76+/-382.75 278.14+/-268.9 N1=40, N2=168 Fold Change: 2.1 P-value: .00012	X	X	X	485.72+/-385.82 206.94+/-269.35 N1=40, N2=10 Fold Change: 3.02 P-value: .02186
35	62	AA147751	480.16+/-205.12 247.19+/-214.23 N1=40, N2=168 Fold Change: 2.38 P-value: 0	X	X	478.2+/-207.42 284.09+/-237.65 N1=40, N2=31 Fold Change: 2.21 P-value: .00015	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
36	**63**	**AA147884**	46.57+/-54.48 235.82+/-200.06 N1=40, N2=168 Fold Change: 4.33 P-value: 0	X	X	X	X
37	**64**	**AA149312**	377.26+/-139.17 193.77+/-99.25 N1=40, N2=168 Fold Change: 2.04 P-value: 0	X	X	374+/-139.43 170.47+/-78.83 N1=40, N2=31 Fold Change: 2.29 P-value: 0	374+/-139.43 140.83+/-37.98 N1=40, N2=10 Fold Change: 2.57 P-value: 0
38	**65**	**AA150501**	213.29+/-103.88 89.09+/-51.7 N1=40, N2=168 Fold Change: 2.45 P-value: 0	X	215.8+/-104 97.8+/-28.03 N1=40, N2=6 Fold Change: 2.01 P-value: .00034	215.8+/-104 74.57+/-38.51 N1=40, N2=31 Fold Change: 2.85 P-value: 0	215.8+/-104 41.35+/-30.37 N1=40, N2=10 Fold Change: 4.75 P-value: 0
39	**66**	**AA151346**	X	X	X	180.8+/-85.07 392.04+/-178.92 N1=39, N2=31 Fold Change: 2.13 P-value: 0	X
40	**68**	**AA155914**	400.19+/-405.95 143.7+/-119.6 N1=40, N2=168 Fold Change: 2.56 P-value: 0	X	X	407.07+/-408.89 135.07+/-104.23 N1=40, N2=31 Fold Change: 2.69 P-value: .00009	X
41	**69**	**AA155952**	X	X	X	343.72+/-239.12 136.91+/-62.46 N1=40, N2=31 Fold Change: 2.23 P-value: 0	343.72+/-239.12 111.1+/-55.68 N1=40, N2=10 Fold Change: 2.77 P-value: .00005
42	**71**	**AA158731**	288.7+/-238.19 93.33+/-144.72 N1=40, N2=168 Fold Change: 3.48 P-value: 0	X	X	287.72+/-241.22 95.77+/-117.6 N1=40, N2=31 Fold Change: 3.08 P-value: .00001	287.72+/-241.22 183.13+/-413.53 N1=40, N2=10 Fold Change: 3.9 P-value: .01612

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
43	73	AA165701	176.56+/-116.87 335.74+/-147.31 N1=40, N2=168 Fold Change: 2.21 P-value: 0	X	176.56+/-116.87 322.48+/-173.1 N1=40, N2=6 Fold Change: 2.14 P-value: .0095	176.56+/-116.87 299.01+/-131.22 N1=40, N2=31 Fold Change: 2.01 P-value: .00002	176.56+/-116.87 309.98+/-142.67 N1=40, N2=10 Fold Change: 2.05 P-value: .00163
44	74	AA166620	227.06+/-165.92 100.03+/-194.31 N1=39, N2=168 Fold Change: 2.58 P-value: 0	X	227.06+/-165.92 88.27+/-25.59 N1=39, N2=10 Fold Change: 2.06 P-value: .00143	227.06+/-165.92 85.25+/-119.41 N1=39, N2=31 Fold Change: 2.98 P-value: 0	227.06+/-165.92 38.81+/-22.68 N1=39, N2=6 Fold Change: 4.89 P-value: 0
45	75	AA173572	368.06+/-171.39 132.7+/-121.15 N1=40, N2=168 Fold Change: 3.31 P-value: 0	X	X	368.73+/-173.58 105.87+/-79.3 N1=40, N2=31 Fold Change: 3.94 P-value: 0	368.73+/-173.58 162.1+/-222.38 N1=40, N2=10 Fold Change: 3.72 P-value: .0091
46	77	AA188763	109.78+/-67.46 223.51+/-105.81 N1=40, N2=168 Fold Change: 2.13 P-value: 0	X	X	X	109.94+/-68.33 210.03+/-82.61 N1=40, N2=10 Fold Change: 2.06 P-value: .00159
47	78	AA193340	X	X	X	338.82+/-318.56 135.54+/-138.52 N1=40, N2=31 Fold Change: 2.47 P-value: .00001	338.82+/-318.56 65.09+/-44.54 N1=40, N2=10 Fold Change: 4.45 P-value: .00006
48	85	AA211369	X	X	X	X	495.8+/-374.32 166.56+/-142.09 N1=40, N2=10 Fold Change: 2.75 P-value: .00161
49	88	AA227778	250.35+/-164.31 103.23+/-228.68 N1=40, N2=168 Fold Change: 3.07 P-value: 0	X	X	254.32+/-164.5 157.31+/-463.97 N1=40, N2=31 Fold Change: 3.09 P-value: .00002	254.32+/-164.5 92.7+/-116.55 N1=40, N2=10 Fold Change: 2.93 P-value: .00666

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
50	95	AA295451	X	X	X	428.38+/-345.54 191.85+/-157.04 N1=40, N2=31 Fold Change: 2.05 P-value: .0027	X
51	96	AA310786	X	X	X	242.07+/-109.49 509.52+/-191.41 N1=40, N2=31 Fold Change: 2.19 P-value: 0	242.07+/-109.49 578.59+/-173.41 N1=40, N2=10 Fold Change: 2.55 P-value: 0
52	97	AA312905	X	X	X	270.53+/-105.99 554.04+/-183.58 N1=40, N2=31 Fold Change: 2.06 P-value: 0	X
53	99	AA369887	X	X	X	X	326.24+/-259.48 88.98+/-90.46 N1=40, N2=10 Fold Change: 4.05 P-value: .00073
54	102	AA400080	X	X	X	89.66+/-112.79 246.79+/-233.75 N1=40, N2=31 Fold Change: 2.21 P-value: .0043	X
55	104	AA417813	846.09+/-411.44 570.86+/-624.96 N1=40, N2=168 Fold Change: 2.01 P-value: 0	X	X	849.01+/-416.4 499.89+/-596.68 N1=40, N2=31 Fold Change: 2.44 P-value: .00007	X
56	106	AA418636	244.96+/-112.2 85.16+/-53.2 N1=39, N2=168 Fold Change: 2.92 P-value: 0	X	244.96+/-112.2 107.39+/-80.98 N1=39, N2=10 Fold Change: 2.43 P-value: .02032	244.96+/-112.2 62.82+/-36.83 N1=39, N2=31 Fold Change: 3.75 P-value: 0	244.96+/-112.2 57.15+/-13.69 N1=39, N2=6 Fold Change: 3.86 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
57	107	AA418995	X	X	X	X	276.52+/-180.68 89.94+/-34.01 N1=40, N2=10 Fold Change: 2.64 P-value: 0
58	109	AA419263	X	X	X	X	547.83+/-148.39 268.37+/-114.78 N1=40, N2=10 Fold Change: 2.12 P-value: .00021
59	112	AA424160	72.76+/-123.26 241.99+/-260.32 N1=40, N2=168 Fold Change: 3.39 P-value: 0	X	X	73.82+/-124.68 344.26+/-347.34 N1=40, N2=31 Fold Change: 5.08 P-value: 0	73.82+/-124.68 405.04+/-245.91 N1=40, N2=10 Fold Change: 7.49 P-value: 0
60	115	AA429308	242.38+/-144.29 124.83+/-150.06 N1=40, N2=168 Fold Change: 2.04 P-value: 0	X	X	237.83+/-143.23 88.15+/-43.75 N1=40, N2=31 Fold Change: 2.47 P-value: 0	237.83+/-143.23 65.39+/-41.56 N1=40, N2=10 Fold Change: 3.5 P-value: .00009
61	116	AA430300	X	X	X	X	511.45+/-201.77 242.83+/-223.58 N1=40, N2=10 Fold Change: 2.55 P-value: .00275
62	117	AA430314	265.86+/-187.91 65.06+/-109.36 N1=40, N2=168 Fold Change: 3.88 P-value: 0	X	X	259.57+/-186.05 59.77+/-101.82 N1=40, N2=31 Fold Change: 4.16 P-value: 0	259.57+/-186.05 -4.03+/-59 N1=40, N2=10 Fold Change: 6.66 P-value: 0
63	118	AA436185	X	X	X	253.53+/-335.89 70.15+/-61.86 N1=40, N2=31 Fold Change: 2.38 P-value: .00089	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
64	119	AA436250	X	X	X	213.31+/-226.04 84.53+/-80.67 N1=40, N2=31 Fold Change: 2.03 P-value: .00323	X
65	120	AA447015	227.33+/-171.55 82.62+/-74.49 N1=40, N2=168 Fold Change: 2.51 P-value: 0	X	X	226.67+/-173.74 66.02+/-51.23 N1=40, N2=31 Fold Change: 2.87 P-value: 0	X
66	122	AA450090	285.47+/-226.15 133.85+/-131.49 N1=40, N2=168 Fold Change: 2.57 P-value: 0	X	X	285.47+/-226.15 125.82+/-152.5 N1=40, N2=31 Fold Change: 2.88 P-value: 0	X
67	124	AA452295	227.07+/-122.52 44.21+/-53.65 N1=40, N2=168 Fold Change: 5.1 P-value: 0	X	220.36+/-116.43 97.66+/-165.2 N1=40, N2=6 Fold Change: 3.73 P-value: .03669	220.36+/-116.43 39.86+/-35.12 N1=40, N2=31 Fold Change: 5.14 P-value: 0	220.36+/-116.43 45.22+/-26.99 N1=40, N2=10 Fold Change: 4.25 P-value: 0
68	125	AA455877	X	X	X	295.74+/-130.76 131.5+/-76.16 N1=40, N2=31 Fold Change: 2.4 P-value: 0	295.74+/-130.76 102.29+/-56 N1=40, N2=10 Fold Change: 3.08 P-value: .0007
69	126	AA456099	X	X	X	X	375.25+/-161.56 163.63+/-115.97 N1=40, N2=10 Fold Change: 2.5 P-value: .00094
70	128	AA464792	X	X	X	X	244.42+/-163.62 77.5+/-57.57 N1=40, N2=10 Fold Change: 2.92 P-value: .00105

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
71	129	AA479033	104.1+/-260.94 492.38+/-952.15 N1=40, N2=168 Fold Change: 2.62 P-value: .00001	X	X	X	X
72	131	AA480075	331.51+/-157.28 155.12+/-117.94 N1=40, N2=168 Fold Change: 2.34 P-value: 0	X	X	331.5+/-159.34 119.29+/-99.73 N1=40, N2=31 Fold Change: 3.04 P-value: 0	331.5+/-159.34 97.24+/-36.96 N1=40, N2=10 Fold Change: 3.11 P-value: 0
73	133	AA486366	237.55+/-149.6 115.8+/-122.37 N1=39, N2=168 Fold Change: 2.09 P-value: 0	X	X	237.55+/-149.6 102.26+/-105.5 N1=39, N2=31 Fold Change: 2.18 P-value: .0001	237.55+/-149.6 20.97+/-35.35 N1=39, N2=6 Fold Change: 4.64 P-value: 0
74	135	AA488889	298.27+/-192.46 99.12+/-55.38 N1=40, N2=168 Fold Change: 2.64 P-value: 0	X	X	298.86+/-194.94 90.94+/-37.43 N1=40, N2=31 Fold Change: 2.8 P-value: 0	298.86+/-194.94 118.43+/-135.55 N1=40, N2=10 Fold Change: 2.62 P-value: .00133
75	136	AA496142	X	X	X	223+/-72.35 113.96+/-51.66 N1=39, N2=31 Fold Change: 2.03 P-value: 0	X
76	137	AA501987	202.15+/-87.72 123.46+/-65.5 N1=39, N2=168 Fold Change: 1.68 P-value: 0	X	X	X	X
77	138	AA502943	438.99+/-109.54 262.83+/-186.3 N1=40, N2=168 Fold Change: 2.11 P-value: 0	X	X	439.24+/-110.96 250.93+/-145.84 N1=40, N2=31 Fold Change: 2.17 P-value: .00002	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
78	139	AA504253	X	X	X	X	394.39+/-105.44 151.15+/-69.52 N1=40, N2=10 Fold Change: 2.81 P-value: .00011
79	140	AA508196	475.57+/-315.6 223.41+/-148.84 N1=40, N2=168 Fold Change: 2.02 P-value: 0	X	X	475.57+/-315.6 207.81+/-174.35 N1=40, N2=31 Fold Change: 2.39 P-value: .00002	475.57+/-315.6 184.11+/-120.65 N1=40, N2=10 Fold Change: 2.51 P-value: .00343
80	141	AA513002	156.4+/-98.44 285.99+/-134.83 N1=39, N2=168 Fold Change: 2.05 P-value: 0	X	X	156.4+/-98.44 282.09+/-129.91 N1=39, N2=31 Fold Change: 2.03 P-value: .00001	X
81	146	AA524095	X	X	X	X	1037.85+/-287.66 517.53+/-221.07 N1=40, N2=10 Fold Change: 2.08 P-value: .00018
82	147	AA524250	337.9+/-133.73 180.07+/-116.79 N1=40, N2=168 Fold Change: 2.02 P-value: 0	X	X	340.18+/-134.68 149.6+/-62.5 N1=40, N2=31 Fold Change: 2.28 P-value: 0	340.18+/-134.68 98.23+/-47.07 N1=40, N2=10 Fold Change: 3.58 P-value: .00001
83	148	AA524536	304.34+/-210.76 116.11+/-126.7 N1=40, N2=168 Fold Change: 2.64 P-value: .00001	X	298.68+/-210.41 87.05+/-113.19 N1=40, N2=6 Fold Change: 3 P-value: .03651	298.68+/-210.41 113.27+/-115.65 N1=40, N2=31 Fold Change: 2.42 P-value: .00101	X
84	151	AA526961	415.49+/-234.41 178.69+/-118.79 N1=40, N2=168 Fold Change: 2.31 P-value: 0	X	X	417.14+/-237.24 163.41+/-149.82 N1=40, N2=31 Fold Change: 2.62 P-value: 0	417.14+/-237.24 119.79+/-62.48 N1=40, N2=10 Fold Change: 3.37 P-value: .00007

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
85	153	AA527180	X	X	X	X	336.44+/-180.05 159.84+/-85.84 N1=40, N2=10 Fold Change: 2.03 P-value: .00507
86	154	AA527298	121.15+/-82.59 287.83+/-242.33 N1=39, N2=168 Fold Change: 1.92 P-value: 0	X	X	X	X
87	155	AA533272	X	X	X	345.7+/-116.17 171.66+/-72 N1=40, N2=31 Fold Change: 2.1 P-value: 0	X
88	159	AA534724	X	X	X	143.93+/-57.72 325.98+/-117.74 N1=40, N2=31 Fold Change: 2.31 P-value: 0	143.93+/-57.72 353.03+/-109.1 N1=40, N2=10 Fold Change: 2.56 P-value: 0
89	160	AA535218	323.08+/-135.81 155.95+/-97.92 N1=40, N2=168 Fold Change: 2.27 P-value: 0	X	X	322.09+/-137.43 178.24+/-126.11 N1=40, N2=31 Fold Change: 2.06 P-value: .00002	X
90	163	AA543076	X	X	X	109.8+/-95.15 365.31+/-441.38 N1=40, N2=31 Fold Change: 2.58 P-value: .00003	X
91	165	AA555312	X	X	X	X	215.48+/-192.29 40.38+/-31.93 N1=40, N2=10 Fold Change: 3.68 P-value: .00006

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
92	169	AA568397	243.4+/-227.66 92.45+/-68.55 N1=40, N2=168 Fold Change: 2.27 P-value: 0	X	243.4+/-227.66 86.44+/-37.31 N1=40, N2=6 Fold Change: 2.12 P-value: .00208	243.4+/-227.66 74.95+/-70.23 N1=40, N2=31 Fold Change: 2.77 P-value: 0	243.4+/-227.66 52.06+/-33.54 N1=40, N2=10 Fold Change: 3.85 P-value: .00005
93	170	AA570519	200.18+/-172.78 77.04+/-65.26 N1=40, N2=168 Fold Change: 2.26 P-value: 0	X	X	X	200.18+/-172.78 48.77+/-33 N1=40, N2=10 Fold Change: 3.04 P-value: .00005
94	171	AA584310	398.21+/-320.55 1296.13+/-716.97 N1=40, N2=168 Fold Change: 3.84 P-value: 0	X	X	402.55+/-323.55 1058.09+/-583.59 N1=40, N2=31 Fold Change: 3.12 P-value: 0	402.55+/-323.55 1089.78+/-475.55 N1=40, N2=10 Fold Change: 3.31 P-value: .00032
95	172	AA584403	593.26+/-1291.79 85.5+/-209.13 N1=40, N2=168 Fold Change: 3.61 P-value: 0	X	X	593.26+/-1291.79 113.63+/-199.33 N1=40, N2=31 Fold Change: 2.7 P-value: .00077	593.26+/-1291.79 77.07+/-76.22 N1=40, N2=10 Fold Change: 3.14 P-value: .00412
96	174	AA595800	X	X	X	405.39+/-344.1 167.2+/-159.75 N1=40, N2=31 Fold Change: 2.2 P-value: .00334	X
97	176	AA602521	X	X	X	X	258.64+/-109.45 92.33+/-57.89 N1=39, N2=6 Fold Change: 3.01 P-value: .00015
98	178	AA609310	289.22+/-160.55 106.23+/-108.02 N1=40, N2=168 Fold Change: 3.16 P-value: 0	X	X	285.39+/-160.8 81.33+/-54.9 N1=40, N2=31 Fold Change: 3.57 P-value: 0	285.39+/-160.8 139.85+/-180.52 N1=40, N2=10 Fold Change: 2.65 P-value: .00931

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
99	180	AA610522	803+/-768.74 2527.25+/-2163.34 N1=40, N2=168 Fold Change: 3.75 P-value: 0	X	803+/-768.74 1730.2+/-869.55 N1=40, N2=6 Fold Change: 3.78 P-value: .00045	803+/-768.74 1878.88+/-1670.25 N1=40, N2=31 Fold Change: 2.57 P-value: .00552	X
100	181	AA612864	X	X	X	228.36+/-116.88 495.29+/-290.05 N1=40, N2=31 Fold Change: 2.03 P-value: 0	228.36+/-116.88 440.68+/-155.22 N1=40, N2=10 Fold Change: 2.03 P-value: .00004
101	184	AA621478	394.08+/-322.25 60.41+/-84.83 N1=40, N2=168 Fold Change: 6.59 P-value: 0	X	398.69+/-325.12 79.9+/-118.32 N1=40, N2=6 Fold Change: 5.51 P-value: .00526	398.69+/-325.12 53.41+/-82.79 N1=40, N2=31 Fold Change: 7.48 P-value: 0	398.69+/-325.12 18+/-20.91 N1=40, N2=10 Fold Change: 11.4 P-value: 0
102	185	AA625387	X	X	X	92.36+/-35.34 208.73+/-105.36 N1=39, N2=31 Fold Change: 2.15 P-value: 0	92.36+/-35.34 231.14+/-178.29 N1=39, N2=6 Fold Change: 2.24 P-value: .00162
103	189	AA628467	1150.97+/-497.25 290.19+/-235.1 N1=40, N2=168 Fold Change: 4.65 P-value: 0	X	X	1145.06+/-502.33 274.87+/-259.13 N1=40, N2=31 Fold Change: 4.99 P-value: 0	1145.06+/-502.33 122.9+/-92.36 N1=40, N2=10 Fold Change: 9.81 P-value: 0
104	192	AA631215	X	X	X	190.98+/-126.92 541.33+/-898.12 N1=40, N2=31 Fold Change: 2.05 P-value: .00057	X
105	193	AA633203	127.67+/-220.56 389.82+/-388.38 N1=40, N2=168 Fold Change: 3.74 P-value: 0	X	X	130.61+/-222.66 451.59+/-365.56 N1=40, N2=31 Fold Change: 5.08 P-value: 0	130.61+/-222.66 413.97+/-273.89 N1=40, N2=10 Fold Change: 4.59 P-value: .00196

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
106	194	AA634799	763.44+/-619.75 367.84+/-431.55 N1=40, N2=168 Fold Change: 2.41 P-value: .00001	X	X	739.38+/-608.62 440.74+/-650.81 N1=40, N2=31 Fold Change: 2.26 P-value: .00284	X
107	196	AA658561	X	X	X	X	238.89+/-114.83 110.57+/-54.76 N1=40, N2=10 Fold Change: 2.02 P-value: .00612
108	198	AA669106	82.72+/-129.9 292.67+/-186.26 N1=40, N2=168 Fold Change: 4.65 P-value: 0	X	X	84.29+/-131.22 383.96+/-227.86 N1=40, N2=31 Fold Change: 6.02 P-value: 0	84.29+/-131.22 381.34+/-202.47 N1=40, N2=10 Fold Change: 6.04 P-value: 0
109	200	AA700621	467.51+/-455.09 66.85+/-123.51 N1=40, N2=168 Fold Change: 6.01 P-value: 0	X	467.51+/-455.09 87.68+/-141.47 N1=40, N2=6 Fold Change: 4.72 P-value: .02358	467.51+/-455.09 36.61+/-66.8 N1=40, N2=31 Fold Change: 7.35 P-value: 0	467.51+/-455.09 26.41+/-35.67 N1=40, N2=10 Fold Change: 8.68 P-value: 0
110	204	AA703262	X	X	X	1213.89+/-750.28 519.38+/-282.83 N1=40, N2=31 Fold Change: 2.09 P-value: .00044	1213.89+/-750.28 361.77+/-193.77 N1=40, N2=10 Fold Change: 3.02 P-value: .00125
111	214	AA742697	1009.7+/-1062.61 222.47+/-326.55 N1=40, N2=168 Fold Change: 4.19 P-value: 0	X	X	1026.03+/-1071.41 238.53+/-383.92 N1=40, N2=31 Fold Change: 4.18 P-value: .00001	1026.03+/-1071.41 142.42+/-134 N1=40, N2=10 Fold Change: 5.09 P-value: .00012
112	215	AA747315	X	X	X	448.86+/-190.26 258.21+/-198.98 N1=40, N2=31 Fold Change: 2.02 P-value: .00001	448.86+/-190.26 135.53+/-84.89 N1=40, N2=10 Fold Change: 3.66 P-value: .0001

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
113	216	AA760767	100.23+/-83.19 245.71+/-246.25 N1=40, N2=168 Fold Change: 2.06 P-value: 0	X	X	101.93+/-83.58 273.79+/-236.49 N1=40, N2=31 Fold Change: 2.59 P-value: .00001	101.93+/-83.58 388.04+/-242.5 N1=40, N2=10 Fold Change: 3.64 P-value: .00384
114	218	AA772278	X	X	X	X	137.98+/-96.56 296.31+/-168.39 N1=40, N2=10 Fold Change: 2.42 P-value: .00585
115	220	AA775180	X	X	X	X	264.55+/-193.81 84.64+/-55.48 N1=40, N2=10 Fold Change: 2.66 P-value: .00029
116	223	AA777369	X	X	X	104.24+/-57.98 211.86+/-128.62 N1=40, N2=31 Fold Change: 2.02 P-value: 0	X
117	226	AA779795	X	X	X	X	493.39+/-168.5 227.18+/-95.72 N1=40, N2=10 Fold Change: 2.25 P-value: .00072
118	227	AA788946	568.73+/-336.98 1313.01+/-867.03 N1=39, N2=168 Fold Change: 2.15 P-value: 0	X	X	X	X
119	228	AA789332	120.94+/-61.86 221.57+/-96.99 N1=39, N2=168 Fold Change: 1.91 P-value: 0	X	X	120.94+/-61.86 228.17+/-103.03 N1=39, N2=31 Fold Change: 1.94 P-value: .00007	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
120	230	AA807154	271.93+/-107.94 150.18+/-94.12 N1=40, N2=168 Fold Change: 2.01 P-value: 0	X	X	273.39+/-108.95 115.85+/-82.09 N1=40, N2=31 Fold Change: 2.55 P-value: 0	273.39+/-108.95 137.82+/-101.26 N1=40, N2=10 Fold Change: 2.3 P-value: .00953
121	235	AA830844	93.3+/-120.3 272.03+/-321.32 N1=40, N2=168 Fold Change: 2.64 P-value: 0	X	X	94.7+/-121.54 320.78+/-455.06 N1=40, N2=31 Fold Change: 2.9 P-value: .00003	94.7+/-121.54 361.79+/-369.37 N1=40, N2=10 Fold Change: 3.88 P-value: .00167
122	236	AA838843	X	X	X	X	1133.4+/-889.08 503.96+/-209.26 N1=40, N2=10 Fold Change: 2 P-value: .00069
123	239	AA846091	83.83+/-80.09 254.24+/-227.12 N1=40, N2=168 Fold Change: 2.88 P-value: 0	X	84.12+/-81.11 271.23+/-192.47 N1=40, N2=6 Fold Change: 3.44 P-value: .01151	84.12+/-81.11 226.57+/-179.06 N1=40, N2=31 Fold Change: 2.75 P-value: 0	X
124	241	AA875998	X	X	X	X	144.49+/-132.98 225.7+/-97.08 N1=40, N2=10 Fold Change: 2.02 P-value: .00162
125	246	AA909042	X	X	X	166.1+/-92.52 345.62+/-200.16 N1=40, N2=31 Fold Change: 2.07 P-value: 0	166.1+/-92.52 375.51+/-207.38 N1=40, N2=10 Fold Change: 2.2 P-value: .00481
126	249	AA909958	X	X	X	304.09+/-148.66 159.71+/-101.37 N1=40, N2=31 Fold Change: 2.04 P-value: .00003	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
127	251	AA913079	X	X	X	X	379.55+/-192 819.72+/-391.8 N1=40, N2=10 Fold Change: 2.18 P-value: .00102
128	254	AA921830	91.7+/-113.88 226.43+/-153.69 N1=40, N2=168 Fold Change: 2.9 P-value: 0	X	X	92.93+/-115.1 257.36+/-191.81 N1=40, N2=31 Fold Change: 3.24 P-value: 0	92.93+/-115.1 324.58+/-186.68 N1=40, N2=10 Fold Change: 4 P-value: .0002
129	255	AA921922	312.62+/-288.86 76.08+/-72.69 N1=40, N2=168 Fold Change: 4.16 P-value: 0	X	X	312.44+/-292.63 75.75+/-54.61 N1=40, N2=31 Fold Change: 3.86 P-value: 0	312.44+/-292.63 36.4+/-15.92 N1=40, N2=10 Fold Change: 6.83 P-value: 0
130	257	AA928698	X	X	X	X	979.86+/-357.7 383.02+/-284.05 N1=40, N2=10 Fold Change: 3.22 P-value: .00199
131	258	AA928776	334.78+/-156.59 126.01+/-82.79 N1=39, N2=168 Fold Change: 2.72 P-value: 0	X	X	334.78+/-156.59 129.6+/-115.01 N1=39, N2=31 Fold Change: 2.74 P-value: 0	334.78+/-156.59 91.05+/-43.12 N1=39, N2=6 Fold Change: 3.62 P-value: .00002
132	259	AA928876	X	X	X	279.93+/-242.15 118.83+/-118.61 N1=40, N2=31 Fold Change: 2.37 P-value: .00023	X
133	260	AA936632	124.77+/-125.66 335.73+/-304.1 N1=40, N2=168 Fold Change: 2.65 P-value: 0	X	X	125.03+/-127.3 307.81+/-176.76 N1=40, N2=31 Fold Change: 2.68 P-value: 0	125.03+/-127.3 325.44+/-181.42 N1=40, N2=10 Fold Change: 3 P-value: .00001

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
134	261	AA947123	288.72+/-99.04 135.96+/-76.03 N1=40, N2=168 Fold Change: 2.34 P-value: 0	X	X	287.11+/-99.81 108.39+/-64.68 N1=40, N2=31 Fold Change: 2.88 P-value: 0	287.11+/-99.81 106.79+/-57.35 N1=40, N2=10 Fold Change: 3.03 P-value: .00116
135	263	AA968657	120.64+/-123.71 221.47+/-188.53 N1=40, N2=168 Fold Change: 2.02 P-value: .00055	X	X	X	X
136	264	AA969863	X	X	X	X	154.92+/-62.69 335+/-158.01 N1=40, N2=10 Fold Change: 2.11 P-value: .00058
137	266	AA976064	363.92+/-151.16 183.7+/-101.29 N1=40, N2=168 Fold Change: 2.17 P-value: 0	X	X	X	X
138	267	AA977204	X	X	X	X	159.24+/-78.21 300.74+/-74.19 N1=40, N2=10 Fold Change: 2.02 P-value: 0
139	272	AB007972	317.37+/-102.68 141.41+/-56.37 N1=40, N2=168 Fold Change: 2.26 P-value: 0	X	X	317.37+/-102.68 127.42+/-50.63 N1=40, N2=31 Fold Change: 2.49 P-value: 0	317.37+/-102.68 110.2+/-25.69 N1=40, N2=10 Fold Change: 2.75 P-value: 0
140	280	AC004010	X	X	X	237.41+/-101.03 119.13+/-50.91 N1=39, N2=31 Fold Change: 2.01 P-value: 0	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
141	281	AC004770	116.54+/-76.22 231.2+/-112.79 N1=40, N2=168 Fold Change: 2.03 P-value: 0	X	X	116.54+/-76.22 258.92+/-95.73 N1=40, N2=31 Fold Change: 2.41 P-value: 0	116.54+/-76.22 353.08+/-90.31 N1=40, N2=10 Fold Change: 3.44 P-value: 0
142	286	AF007150	X	X	X	X	560.67+/-252.85 244.22+/-118.81 N1=40, N2=10 Fold Change: 2.3 P-value: .00021
143	287	AF009314	280.81+/-113.17 138.34+/-66.55 N1=40, N2=168 Fold Change: 2.04 P-value: 0	X	X	X	280.81+/-113.17 90.09+/-43.95 N1=40, N2=10 Fold Change: 3.18 P-value: .00003
144	297	AF052142	307.17+/-169.55 136.07+/-86.42 N1=40, N2=168 Fold Change: 2.28 P-value: 0	X	X	307.17+/-169.55 134.05+/-84.74 N1=40, N2=31 Fold Change: 2.25 P-value: 0	307.17+/-169.55 131.75+/-87.96 N1=40, N2=10 Fold Change: 2.44 P-value: .00309
145	300	AF058075	X	X	X	X	-15.62+/-107.9 355.75+/-489.88 N1=40, N2=10 Fold Change: 3.73 P-value: .0394
146	304	AF070648	1031.52+/-429.52 432.03+/-213.34 N1=40, N2=168 Fold Change: 2.41 P-value: 0	X	X	1031.52+/-429.52 357.01+/-152.1 N1=40, N2=31 Fold Change: 2.82 P-value: 0	1031.52+/-429.52 292.72+/-163.49 N1=40, N2=10 Fold Change: 3.62 P-value: .00002
147	309	AF150174	211.02+/-104.05 86.63+/-46.76 N1=39, N2=168 Fold Change: 2.26 P-value: 0	X	X	211.02+/-104.05 86.92+/-51.98 N1=39, N2=31 Fold Change: 2.26 P-value: 0	211.02+/-104.05 78.32+/-31.52 N1=39, N2=6 Fold Change: 2.38 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
148	311	AI002238	X	X	X	X	254.67+/-91.81 105.29+/-71.62 N1=40, N2=10 Fold Change: 2.72 P-value: .00083
149	314	AI016604	X	X	X	502.7+/-255.95 262.05+/-145.41 N1=40, N2=31 Fold Change: 2.02 P-value: .00002	502.7+/-255.95 226.05+/-112.74 N1=40, N2=10 Fold Change: 2.18 P-value: .00111
150	317	AI018523	422.08+/-187.64 94.36+/-123.53 N1=40, N2=168 Fold Change: 5.56 P-value: 0	X	X	422.08+/-187.64 77.78+/-105.86 N1=40, N2=31 Fold Change: 6.54 P-value: 0	422.08+/-187.64 44.08+/-59.8 N1=40, N2=10 Fold Change: 9.77 P-value: 0
151	321	AI031771	85.9+/-105.07 257.24+/-405.17 N1=40, N2=168 Fold Change: 2.53 P-value: 0	X	X	85.9+/-105.07 298.84+/-697.75 N1=40, N2=31 Fold Change: 2.33 P-value: .00142	X
152	324	AI039005	201.84+/-130.44 77.34+/-61.5 N1=40, N2=168 Fold Change: 2.58 P-value: 0	X	X	203.54+/-131.69 61.56+/-42.38 N1=40, N2=31 Fold Change: 3.03 P-value: 0	203.54+/-131.69 44.43+/-54.48 N1=40, N2=10 Fold Change: 3.97 P-value: .0001
153	325	AI039722	990.63+/-1152.38 438.37+/-1004.04 N1=40, N2=168 Fold Change: 3.87 P-value: 0	X	X	1007.24+/-1162.59 232.49+/-466.94 N1=40, N2=31 Fold Change: 6.17 P-value: 0	1007.24+/-1162.59 207.73+/-245.94 N1=40, N2=10 Fold Change: 5.76 P-value: .00392
154	326	AI049549	653.84+/-535.62 267.97+/-227.53 N1=40, N2=168 Fold Change: 2.36 P-value: 0	X	X	653.84+/-535.62 226.29+/-141.74 N1=40, N2=31 Fold Change: 2.5 P-value: .00001	653.84+/-535.62 155.78+/-116.9 N1=40, N2=10 Fold Change: 3.66 P-value: .00006

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
155	327	AI049973	X	X	X	X	391.85+/-108.68 199.36+/-52.62 N1=39, N2=6 Fold Change: 1.95 P-value: .00002
156	330	AI056241	241.39+/-152.04 67.68+/-55.35 N1=39, N2=168 Fold Change: 2.88 P-value: 0	X	241.39+/-152.04 93.33+/-104.89 N1=39, N2=10 Fold Change: 2.9 P-value: .03101	241.39+/-152.04 49.94+/-43.13 N1=39, N2=31 Fold Change: 3.33 P-value: 0	241.39+/-152.04 45.49+/-48.07 N1=39, N2=6 Fold Change: 4.03 P-value: .00003
157	331	AI057450	381.32+/-1572.07 20.72+/-180.68 N1=40, N2=168 Fold Change: 2.92 P-value: .00006	X	X	381.32+/-1572.07 27.5+/-176.72 N1=40, N2=31 Fold Change: 2.87 P-value: .00026	381.32+/-1572.07 10.16+/-47.15 N1=40, N2=10 Fold Change: 2.99 P-value: .00095
158	332	AI057637	568.22+/-502.47 153.6+/-81.89 N1=40, N2=168 Fold Change: 3.29 P-value: 0	X	573.52+/-507.9 163.69+/-59.04 N1=40, N2=6 Fold Change: 2.9 P-value: .0001	573.52+/-507.9 129.31+/-59.91 N1=40, N2=31 Fold Change: 3.79 P-value: 0	573.52+/-507.9 124.36+/-39.47 N1=40, N2=10 Fold Change: 3.81 P-value: 0
159	336	AI078033	454.77+/-280.5 203.08+/-158.36 N1=40, N2=168 Fold Change: 2.27 P-value: 0	X	X	454.77+/-280.5 183.47+/-128.31 N1=40, N2=31 Fold Change: 2.42 P-value: 0	454.77+/-280.5 129.56+/-78.11 N1=40, N2=10 Fold Change: 3.22 P-value: .00008
160	337	AI078121	267.92+/-121.01 129.6+/-75.04 N1=39, N2=168 Fold Change: 2.01 P-value: 0	X	X	X	267.92+/-121.01 124.52+/-39.11 N1=39, N2=6 Fold Change: 2.05 P-value: .00004
161	338	AI079545	X	X	248.94+/-138.38 463.39+/-104.61 N1=40, N2=6 Fold Change: 2.14 P-value: .00004	X	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
162	339	AI079558	X	X	X	115.76+/-141.71 214.96+/-122.84 N1=40, N2=31 Fold Change: 2.3 P-value: .00001	X
163	341	AI083598	344.81+/-287.52 151.49+/-429.97 N1=40, N2=168 Fold Change: 3.75 P-value: 0	X	X	339.56+/-289.33 210.77+/-736.98 N1=40, N2=31 Fold Change: 4.41 P-value: 0	339.56+/-289.33 31.3+/-28.36 N1=40, N2=10 Fold Change: 6.76 P-value: 0
164	342	AI086614	300.02+/-151.08 127.26+/-88.54 N1=40, N2=168 Fold Change: 2.5 P-value: 0	X	X	301.2+/-152.86 96.79+/-68.03 N1=40, N2=31 Fold Change: 3.25 P-value: 0	301.2+/-152.86 68.08+/-44.9 N1=40, N2=10 Fold Change: 3.7 P-value: 0
165	343	AI087975	137.52+/-92.28 277.44+/-204.79 N1=39, N2=168 Fold Change: 1.96 P-value: 0	X	X	X	X
166	344	AI088609	711.92+/-592.71 327.21+/-706.4 N1=40, N2=168 Fold Change: 3.75 P-value: 0	X	X	709.25+/-600.21 163.7+/-218.98 N1=40, N2=31 Fold Change: 4.73 P-value: 0	709.25+/-600.21 78.97+/-52.81 N1=40, N2=10 Fold Change: 6.93 P-value: 0
167	345	AI091154	351.29+/-406.17 73.95+/-133.05 N1=40, N2=168 Fold Change: 4.29 P-value: 0	X	351.29+/-406.17 87.21+/-103.53 N1=40, N2=6 Fold Change: 3.04 P-value: .0365	351.29+/-406.17 86.99+/-153.12 N1=40, N2=31 Fold Change: 3.61 P-value: 0	351.29+/-406.17 62.86+/-69.84 N1=40, N2=10 Fold Change: 3.91 P-value: .00107
168	346	AI092936	185.51+/-150.9 417.08+/-227.5 N1=40, N2=168 Fold Change: 2.2 P-value: 0	X	X	186.98+/-152.58 425.95+/-204.95 N1=40, N2=31 Fold Change: 2.35 P-value: .00001	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
169	348	AI094535	204.98+/-121.07 348.38+/-182.49 N1=39, N2=168 Fold Change: 1.75 P-value: .00003	X	X	X	X
170	349	AI096389	X	X	X	X	354.78+/-131.25 184.82+/-126.35 N1=40, N2=10 Fold Change: 2.08 P-value: .00216
171	351	AI123555	300.32+/-162.49 75.22+/-66.82 N1=40, N2=168 Fold Change: 4.19 P-value: 0	X	300+/-164.6 91.12+/-67 N1=40, N2=6 Fold Change: 3.22 P-value: .00482	300+/-164.6 67.15+/-70.68 N1=40, N2=31 Fold Change: 4.66 P-value: 0	300+/-164.6 55.08+/-36.39 N1=40, N2=10 Fold Change: 4.97 P-value: .00001
172	352	AI123738	297.76+/-110.04 156.35+/-127.73 N1=39, N2=168 Fold Change: 2.06 P-value: 0	X	X	297.76+/-110.04 152.58+/-82.32 N1=39, N2=31 Fold Change: 2.04 P-value: 0	297.76+/-110.04 120.8+/-50.92 N1=39, N2=6 Fold Change: 2.46 P-value: .00002
173	355	AI125252	69.28+/-126.42 217.42+/-192.92 N1=39, N2=168 Fold Change: 2.31 P-value: 0	X	X	69.28+/-126.42 215.91+/-164.16 N1=39, N2=31 Fold Change: 2.27 P-value: .00023	X
174	357	AI126237	X	X	X	X	220.92+/-142.18 366.48+/-123.56 N1=40, N2=10 Fold Change: 2.01 P-value: .00008
175	358	AI127289	X	X	X	230.52+/-149.31 872.58+/-881.67 N1=40, N2=31 Fold Change: 2.85 P-value: .00002	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
176	359	AI128820	225.63+/-90.11 101.84+/-66.82 N1=40, N2=168 Fold Change: 2.29 P-value: 0	X	X	224.42+/-90.96 96.42+/-39.89 N1=40, N2=31 Fold Change: 2.29 P-value: 0	224.42+/-90.96 82.27+/-38.37 N1=40, N2=10 Fold Change: 2.85 P-value: .0008
177	360	AI129320	462.88+/-248.98 223.69+/-111.28 N1=40, N2=168 Fold Change: 2.08 P-value: 0	X	X	462.06+/-252.18 218.45+/-156.49 N1=40, N2=31 Fold Change: 2.3 P-value: 0	462.06+/-252.18 242.37+/-237.11 N1=40, N2=10 Fold Change: 2.23 P-value: .00458
178	362	AI131078	299.48+/-223.81 105.31+/-56.6 N1=40, N2=168 Fold Change: 2.51 P-value: 0	X	X	299.48+/-223.81 102.41+/-57.3 N1=40, N2=31 Fold Change: 2.6 P-value: 0	299.48+/-223.81 99.18+/-37.7 N1=40, N2=10 Fold Change: 2.48 P-value: .00001
179	365	AI140764	241.9+/-66.27 127.44+/-57.54 N1=39, N2=168 Fold Change: 2.03 P-value: 0	X	X	X	241.9+/-66.27 119.16+/-48.86 N1=39, N2=6 Fold Change: 2.11 P-value: .00026
180	367	AI141556	X	X	X	X	297.58+/-90.49 101.69+/-39.39 N1=40, N2=10 Fold Change: 2.97 P-value: 0
181	368	AI144477	560.95+/-250.34 250.3+/-192.18 N1=40, N2=168 Fold Change: 2.61 P-value: 0	X	X	564.89+/-252.35 332.2+/-275.56 N1=40, N2=31 Fold Change: 2.04 P-value: .00003	X
182	370	AI148006	241.32+/-191.01 84.05+/-116.71 N1=40, N2=168 Fold Change: 2.99 P-value: 0	X	X	241.17+/-193.5 51.87+/-67.91 N1=40, N2=31 Fold Change: 4.03 P-value: 0	241.17+/-193.5 25.24+/-42.83 N1=40, N2=10 Fold Change: 5.56 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
183	373	AI149693	223.18+/-91.72 95.74+/-62.93 N1=39, N2=168 Fold Change: 2.5 P-value: 0	X	X	223.18+/-91.72 107.58+/-66.58 N1=39, N2=31 Fold Change: 2.25 P-value: 0	223.18+/-91.72 113.09+/-116.05 N1=39, N2=6 Fold Change: 2.37 P-value: .00396
184	375	AI160811	X	X	X	X	243+/-112.73 111.62+/-39.76 N1=40, N2=10 Fold Change: 2.04 P-value: .00009
185	376	AI161049	301.58+/-452.1 77.97+/-71.53 N1=40, N2=168 Fold Change: 2.61 P-value: .00001	X	X	301.58+/-452.1 76.69+/-52.21 N1=40, N2=31 Fold Change: 2.46 P-value: .00013	301.58+/-452.1 76.68+/-82.57 N1=40, N2=10 Fold Change: 2.77 P-value: .00751
186	378	AI168057	356.99+/-119.9 188.39+/-84.68 N1=39, N2=168 Fold Change: 1.94 P-value: 0	X	X	X	X
187	380	AI189011	X	X	X	X	284.7+/-101.6 127.96+/-60.39 N1=40, N2=10 Fold Change: 2.41 P-value: .00278
188	381	AI189255	X	X	X	X	205.71+/-81.06 101.78+/-59.91 N1=40, N2=10 Fold Change: 2.2 P-value: .00676
189	382	AI190755	X	X	X	290.63+/-103.17 141.14+/-64.83 N1=40, N2=31 Fold Change: 2.13 P-value: 0	290.63+/-103.17 100.98+/-38.82 N1=40, N2=10 Fold Change: 2.9 P-value: .00001

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
190	384	AI200954	529.23+/-316.46 256.1+/-158.56 N1=40, N2=168 Fold Change: 2.07 P-value: 0	X	X	524.84+/-319.36 219.57+/-119.93 N1=40, N2=31 Fold Change: 2.28 P-value: .00001	524.84+/-319.36 165.98+/-93.19 N1=40, N2=10 Fold Change: 3.18 P-value: .00195
191	385	AI201273	535.25+/-296.2 238.85+/-188.24 N1=40, N2=168 Fold Change: 2.5 P-value: 0	X	X	533.25+/-299.79 203.14+/-125.12 N1=40, N2=31 Fold Change: 2.61 P-value: 0	533.25+/-299.79 125.11+/-95.45 N1=40, N2=10 Fold Change: 4.56 P-value: .0001
192	386	AI201965	237.22+/-148.65 107.53+/-70.7 N1=40, N2=168 Fold Change: 2.18 P-value: 0	X	X	234.24+/-149.37 100.47+/-56.35 N1=40, N2=31 Fold Change: 2.19 P-value: .00001	234.24+/-149.37 65.63+/-51.87 N1=40, N2=10 Fold Change: 3.63 P-value: .00031
193	387	AI201982	279.97+/-146.77 114.06+/-74.45 N1=39, N2=168 Fold Change: 2.45 P-value: 0	X	X	279.97+/-146.77 121.58+/-55.99 N1=39, N2=31 Fold Change: 2.14 P-value: 0	279.97+/-146.77 121.2+/-81.62 N1=39, N2=6 Fold Change: 2.51 P-value: .00327
194	388	AI206014	213.72+/-107.69 81.38+/-54.34 N1=40, N2=168 Fold Change: 2.63 P-value: 0	X	X	211.4+/-108.08 80.55+/-42.41 N1=40, N2=31 Fold Change: 2.54 P-value: 0	211.4+/-108.08 60.05+/-31.32 N1=40, N2=10 Fold Change: 3.36 P-value: .00001
195	389	AI206063	133.1+/-160.7 339.26+/-339.95 N1=40, N2=168 Fold Change: 2.57 P-value: .00002	X	X	133.1+/-160.7 353.59+/-366.06 N1=40, N2=31 Fold Change: 2.7 P-value: .00061	X
196	393	AI218358	210.74+/-117.83 87.3+/-105.07 N1=39, N2=168 Fold Change: 2.43 P-value: 0	X	210.74+/-117.83 82.51+/-91.18 N1=39, N2=10 Fold Change: 2.74 P-value: .0333	210.74+/-117.83 76.3+/-97.56 N1=39, N2=31 Fold Change: 2.64 P-value: 0	210.74+/-117.83 74.44+/-133.85 N1=39, N2=6 Fold Change: 3.62 P-value: .00101

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
197	394	AI222594	431.73+/-162.38 169.82+/-117.43 N1=40, N2=168 Fold Change: 2.81 P-value: 0	X	X	431.73+/-162.38 143.7+/-81.33 N1=40, N2=31 Fold Change: 3.23 P-value: 0	X
198	397	AI242160	320.5+/-159.05 170.68+/-74.58 N1=39, N2=168 Fold Change: 1.73 P-value: 0	X	X	X	X
199	398	AI244908	X	X	X	X	425.47+/-356.02 148.1+/-83.25 N1=40, N2=10 Fold Change: 2.51 P-value: .00165
200	399	AI247837	250.33+/-314.52 40.01+/-55.99 N1=40, N2=168 Fold Change: 3.88 P-value: 0	X	X	250.33+/-314.52 34.79+/-48.59 N1=40, N2=31 Fold Change: 4.13 P-value: 0	250.33+/-314.52 20.13+/-36.3 N1=40, N2=10 Fold Change: 4.49 P-value: 0
201	401	AI264135	X	X	X	X	246.38+/-130.33 97.95+/-69.13 N1=40, N2=10 Fold Change: 2.68 P-value: .00126
202	403	AI266650	X	X	X	X	657.85+/-222.05 309.8+/-83.6 N1=40, N2=10 Fold Change: 2.09 P-value: .00001
203	405	AI275140	X	X	X	26.4+/-47.96 232.81+/-210.09 N1=40, N2=31 Fold Change: 6.41 P-value: 0	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
204	**407**	**AI276259**	121.2+/-221.34 238.08+/-274.65 N1=40, N2=168 Fold Change: 2.02 P-value: .00019	X	X	121.51+/-224.22 245.37+/-268.39 N1=40, N2=31 Fold Change: 2.09 P-value: .00466	X
205	**408**	**AI277612**	1009.49+/-899.38 93.86+/-163.03 N1=40, N2=168 Fold Change: 9.23 P-value: 0	X	1022.91+/-907.07 163.73+/-156.36 N1=40, N2=6 Fold Change: 5.12 P-value: .00592	1022.91+/-907.07 82.75+/-117.04 N1=40, N2=31 Fold Change: 10.43 P-value: 0	1022.91+/-907.07 40.07+/-27.26 N1=40, N2=10 Fold Change: 16.08 P-value: 0
206	**413**	**AI285970**	X	X	X	269.01+/-274.71 88.12+/-54.51 N1=40, N2=31 Fold Change: 2 P-value: .00393	X
207	**414**	**AI288586**	X	X	X	313.32+/-139.2 113.39+/-56.77 N1=39, N2=31 Fold Change: 2.6 P-value: 0	313.32+/-139.2 107.36+/-49.96 N1=39, N2=6 Fold Change: 2.94 P-value: .00028
208	**415**	**AI288745**	276.49+/-146.02 108.9+/-73.82 N1=39, N2=168 Fold Change: 2.51 P-value: 0	X	X	276.49+/-146.02 104.75+/-63.19 N1=39, N2=31 Fold Change: 2.5 P-value: 0	276.49+/-146.02 67.42+/-24.06 N1=39, N2=6 Fold Change: 3.69 P-value: 0
209	**417**	**AI300876**	601.83+/-985.51 74.02+/-258.41 N1=40, N2=168 Fold Change: 6.47 P-value: 0	X	X	601.83+/-985.51 54.33+/-149.24 N1=40, N2=31 Fold Change: 6.66 P-value: 0	601.83+/-985.51 13.6+/-22.13 N1=40, N2=10 Fold Change: 8.67 P-value: 0
210	**422**	**AI333767**	X	X	X	X	201.68+/-104.32 104.93+/-75.04 N1=40, N2=10 Fold Change: 2 P-value: .00805

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
211	423	AI333987	X	X	X	208.53+/-320.79 57.06+/-100.56 N1=40, N2=31 Fold Change: 2.4 P-value: .00125	X
212	424	AI338536	X	X	X	X	548.6+/-192.05 227.52+/-68.12 N1=40, N2=10 Fold Change: 2.31 P-value: 0
213	427	AI341602	135.16+/-276.86 593.58+/-944.91 N1=40, N2=168 Fold Change: 4.46 P-value: 0	X	137.44+/-280.1 438.85+/-447.12 N1=40, N2=6 Fold Change: 3.86 P-value: .03152	137.44+/-280.1 723.06+/-652.3 N1=40, N2=31 Fold Change: 6.28 P-value: 0	137.44+/-280.1 580.91+/-380.87 N1=40, N2=10 Fold Change: 6.09 P-value: .00062
214	428	AI342169	X	X	X	X	496.19+/-393.99 1347.53+/-986.09 N1=40, N2=10 Fold Change: 2.64 P-value: .0043
215	430	AI344312	84.72+/-57.63 209.71+/-134.29 N1=40, N2=168 Fold Change: 2.33 P-value: 0	X	X	X	X
216	431	AI346341	640.59+/-422.41 155.96+/-203.21 N1=40, N2=168 Fold Change: 4.26 P-value: 0	X	X	635.18+/-426.52 120.31+/-143.98 N1=40, N2=31 Fold Change: 4.92 P-value: 0	635.18+/-426.52 104.05+/-133.87 N1=40, N2=10 Fold Change: 5.89 P-value: .00006
217	432	AI351043	236.73+/-93.44 109.27+/-56.02 N1=40, N2=168 Fold Change: 2.23 P-value: 0	X	X	236.3+/-94.62 98.05+/-50.78 N1=40, N2=31 Fold Change: 2.47 P-value: 0	236.3+/-94.62 73.16+/-38.18 N1=40, N2=10 Fold Change: 3.35 P-value: .00009

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
218	434	AI352171	X	X	X	222.69+/-144.28 77.49+/-85.14 N1=39, N2=31 Fold Change: 2.28 P-value: 0	222.69+/-144.28 51.96+/-71.13 N1=39, N2=6 Fold Change: 2.86 P-value: .00032
219	436	AI357639	X	X	X	X	103.44+/-82.21 229.26+/-76.25 N1=40, N2=10 Fold Change: 2.51 P-value: 0
220	437	AI361002	X	X	X	226.33+/-66.64 131.77+/-56.91 N1=39, N2=31 Fold Change: 1.8 P-value: 0	209.31+/-66.11 116.1+/-36.28 N1=39, N2=6 Fold Change: 1.82 P-value: .00118
221	441	AI369275	412.08+/-182.64 160.8+/-88.56 N1=40, N2=168 Fold Change: 2.56 P-value: 0	X	X	404.52+/-178.58 156.69+/-71.33 N1=40, N2=31 Fold Change: 2.52 P-value: 0	404.52+/-178.58 124.99+/-48.08 N1=40, N2=10 Fold Change: 3.09 P-value: 0
222	443	AI375115	215.71+/-84.93 107.21+/-43.49 N1=40, N2=168 Fold Change: 2.02 P-value: 0	X	X	211.26+/-81.18 101.07+/-42.95 N1=40, N2=31 Fold Change: 2.07 P-value: 0	211.26+/-81.18 95.25+/-21.17 N1=40, N2=10 Fold Change: 2.08 P-value: 0
223	446	AI377937	X	X	X	360.06+/-360.99 150.11+/-76.77 N1=40, N2=31 Fold Change: 2.07 P-value: .00001	360.06+/-360.99 160.98+/-94.5 N1=40, N2=10 Fold Change: 2 P-value: .0091
224	447	AI378584	837.48+/-393.22 288.6+/-150.82 N1=40, N2=168 Fold Change: 2.77 P-value: 0	X	X	815.22+/-371.96 263.18+/-114.79 N1=40, N2=31 Fold Change: 2.89 P-value: 0	815.22+/-371.96 231+/-80.99 N1=40, N2=10 Fold Change: 3.19 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
225	**448**	**AI379723**	386.86+/-176.47 126.18+/-143.63 N1=40, N2=168 Fold Change: 3.46 P-value: 0	X	380.22+/-173.64 136.6+/-134.47 N1=40, N2=6 Fold Change: 3.5 P-value: .03454	380.22+/-173.64 87.51+/-60.3 N1=40, N2=31 Fold Change: 4.24 P-value: 0	380.22+/-173.64 68.16+/-48.01 N1=40, N2=10 Fold Change: 5.51 P-value: 0
226	**450**	**AI380204**	X	X	X	194.43+/-169.86 361.5+/-246.51 N1=40, N2=31 Fold Change: 2.15 P-value: .00078	X
227	**452**	**AI380932**	X	X	X	X	191.48+/-96.27 387.31+/-138.62 N1=40, N2=10 Fold Change: 2.16 P-value: .00071
228	**456**	**AI381930**	269.91+/-245.06 44.47+/-65.54 N1=39, N2=168 Fold Change: 3.7 P-value: 0	X	269.91+/-245.06 63.86+/-29.55 N1=39, N2=10 Fold Change: 3.2 P-value: .00133	269.91+/-245.06 34.22+/-46.82 N1=39, N2=31 Fold Change: 3.85 P-value: 0	269.91+/-245.06 62.78+/-171.44 N1=39, N2=6 Fold Change: 3.91 P-value: .0021
229	**458**	**AI393356**	X	X	X	74.44+/-64.03 339.43+/-658.29 N1=40, N2=31 Fold Change: 2.18 P-value: .00164	X
230	**461**	**AI401832**	X	X	X	72.16+/-151.56 408.66+/-668.16 N1=40, N2=31 Fold Change: 2.63 P-value: .00745	X
231	**462**	**AI417267**	927.3+/-482.64 259.61+/-119.48 N1=40, N2=168 Fold Change: 3.36 P-value: 0	X	933.35+/-487.41 387.97+/-131.13 N1=40, N2=6 Fold Change: 2.11 P-value: .0003	933.35+/-487.41 238.15+/-85.44 N1=40, N2=31 Fold Change: 3.54 P-value: 0	933.35+/-487.41 240.55+/-123.45 N1=40, N2=10 Fold Change: 3.74 P-value: .00001

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
232	463	AI417917	564.39+/-315.14 271.17+/-167.23 N1=40, N2=168 Fold Change: 2.25 P-value: 0	X	X	567.47+/-318.65 218.33+/-110.93 N1=40, N2=31 Fold Change: 2.61 P-value: 0	567.47+/-318.65 115.26+/-82.27 N1=40, N2=10 Fold Change: 5.16 P-value: .00005
233	465	AI418481	X	X	X	77.52+/-60.1 257.35+/-253.01 N1=40, N2=31 Fold Change: 2.83 P-value: 0	X
234	466	AI418596	X	X	X	X	229.67+/-120.12 43.69+/-43.08 N1=39, N2=6 Fold Change: 3.79 P-value: 0
235	467	AI419030	446.12+/-255.78 158.41+/-132.36 N1=40, N2=168 Fold Change: 3.03 P-value: 0	X	X	445.97+/-259.12 133.67+/-123.4 N1=40, N2=31 Fold Change: 3.56 P-value: 0	445.97+/-259.12 81.99+/-31.49 N1=40, N2=10 Fold Change: 4.69 P-value: 0
236	468	AI421837	294.7+/-145.9 111.04+/-64.19 N1=40, N2=168 Fold Change: 2.62 P-value: 0	X	X	293.96+/-147.73 102.42+/-57.12 N1=40, N2=31 Fold Change: 2.8 P-value: 0	293.96+/-147.73 109.78+/-55.53 N1=40, N2=10 Fold Change: 2.62 P-value: .00166
237	469	AI431799	X	X	463.05+/-382.43 658.8+/-240.03 N1=40, N2=6 Fold Change: 2 P-value: .00993	X	X
238	471	AI435828	X	X	X	587.69+/-414.14 299.14+/-333.14 N1=40, N2=31 Fold Change: 2.52 P-value: .00061	587.69+/-414.14 119.57+/-42.81 N1=40, N2=10 Fold Change: 3.9 P-value: .00001

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
239	475	AI446030	383.04+/-264.2 935.53+/-916.21 N1=40, N2=168 Fold Change: 2.29 P-value: 0	X	X	383.04+/-264.2 987.66+/-795.06 N1=40, N2=31 Fold Change: 2.53 P-value: 0	X
240	476	AI446168	216.67+/-584.58 561.08+/-695.63 N1=40, N2=168 Fold Change: 3.28 P-value: 0	X	X	220.39+/-591.75 606.41+/-908.81 N1=40, N2=31 Fold Change: 3.51 P-value: 0	220.39+/-591.75 603.11+/-527.41 N1=40, N2=10 Fold Change: 3.91 P-value: .00476
241	477	AI458003	276.51+/-201.47 38.41+/-97.2 N1=40, N2=168 Fold Change: 5.07 P-value: 0	X	280.16+/-202.76 81.96+/-89.4 N1=40, N2=6 Fold Change: 3.22 P-value: .03405	280.16+/-202.76 43.42+/-152.26 N1=40, N2=31 Fold Change: 4.35 P-value: 0	280.16+/-202.76 4.43+/-42.79 N1=40, N2=10 Fold Change: 7.36 P-value: 0
242	482	AI468491	X	X	X	X	256.57+/-264.41 84.09+/-113.95 N1=40, N2=10 Fold Change: 2.68 P-value: .00796
243	487	AI480215	122.23+/-104.86 295.22+/-297.68 N1=40, N2=168 Fold Change: 2.15 P-value: .00005	X	X	125.66+/-103.93 321.02+/-262.5 N1=40, N2=31 Fold Change: 2.49 P-value: .0002	X
244	489	AI492051	384.45+/-175.99 157.89+/-176.84 N1=40, N2=168 Fold Change: 3.12 P-value: 0	X	X	382.34+/-177.78 91.96+/-44.92 N1=40, N2=31 Fold Change: 4.08 P-value: 0	382.34+/-177.78 154.08+/-202.28 N1=40, N2=10 Fold Change: 3.91 P-value: .0032
245	490	AI492091	X	X	X	X	146.39+/-59.05 321.61+/-116.38 N1=40, N2=10 Fold Change: 2.22 P-value: .00005

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
246	493	AI492879	214.23+/-650.46 465.24+/-396.65 N1=40, N2=168 Fold Change: 6.22 P-value: 0	X	219.42+/-658.12 277.88+/-265.92 N1=40, N2=6 Fold Change: 3.72 P-value: .01903	219.42+/-658.12 663.74+/-488.43 N1=40, N2=31 Fold Change: 9.89 P-value: 0	219.42+/-658.12 771.71+/-307.65 N1=40, N2=10 Fold Change: 14.12 P-value: 0
247	494	AI498375	244.41+/-203.11 46+/-55.84 N1=39, N2=168 Fold Change: 3.62 P-value: 0	X	244.41+/-203.11 47.6+/-45.95 N1=39, N2=10 Fold Change: 3.32 P-value: .00134	244.41+/-203.11 43.16+/-57.68 N1=39, N2=31 Fold Change: 3.62 P-value: 0	244.41+/-203.11 48.55+/-41.9 N1=39, N2=6 Fold Change: 3.45 P-value: .00002
248	498	AI499334	236.34+/-181.29 117.03+/-221.42 N1=39, N2=168 Fold Change: 2.28 P-value: 0	X	236.34+/-181.29 83.26+/-88.81 N1=39, N2=10 Fold Change: 2.68 P-value: .0244	X	236.34+/-181.29 16.68+/-51.22 N1=39, N2=6 Fold Change: 4.22 P-value: 0
249	500	AI524085	380.84+/-525.16 54.03+/-109.2 N1=40, N2=168 Fold Change: 4.48 P-value: 0	X	388.89+/-529.52 35.06+/-63.65 N1=40, N2=6 Fold Change: 4.76 P-value: .00065	388.89+/-529.52 36.84+/-79.16 N1=40, N2=31 Fold Change: 5.39 P-value: 0	388.89+/-529.52 8.33+/-48.11 N1=40, N2=10 Fold Change: 7 P-value: 0
250	501	AI525044	319.4+/-142.13 131.06+/-178.35 N1=40, N2=168 Fold Change: 2.93 P-value: 0	X	X	316.89+/-143.08 121.55+/-76.85 N1=40, N2=31 Fold Change: 2.83 P-value: 0	316.89+/-143.08 65.73+/-20.84 N1=40, N2=10 Fold Change: 4.61 P-value: 0
251	502	AI525601	X	X	X	X	223.25+/-101.98 605.18+/-406.21 N1=40, N2=10 Fold Change: 2.43 P-value: .00221
252	504	AI535997	526.38+/-278.8 203.43+/-127.91 N1=40, N2=168 Fold Change: 2.55 P-value: 0	X	X	527.18+/-282.39 182.64+/-99.43 N1=40, N2=31 Fold Change: 2.76 P-value: 0	527.18+/-282.39 177.05+/-109.73 N1=40, N2=10 Fold Change: 2.81 P-value: .00005

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
253	506	AI539386	1911.09+/-2400.57 4189.96+/-4852.35 N1=40, N2=168 Fold Change: 2.2 P-value: .00002	X	X	1924.9+/-2430.34 4667.18+/-4736.01 N1=40, N2=31 Fold Change: 2.62 P-value: .00005	X
254	507	AI539443	105.57+/-75.36 244.51+/-212.14 N1=39, N2=168 Fold Change: 2.05 P-value: 0	X	X	105.57+/-75.36 235.02+/-188.35 N1=39, N2=31 Fold Change: 2.11 P-value: .00011	X
255	509	AI546943	X	X	X	X	310.79+/-204.98 120.98+/-130.81 N1=40, N2=10 Fold Change: 3.17 P-value: .01143
256	510	AI553918	831.82+/-279.85 384.25+/-176.84 N1=40, N2=168 Fold Change: 2.22 P-value: 0	X	X	821.96+/-276.38 364.75+/-169.81 N1=40, N2=31 Fold Change: 2.31 P-value: 0	821.96+/-276.38 378.99+/-216.53 N1=40, N2=10 Fold Change: 2.43 P-value: .00313
257	511	AI554514	X	X	90.74+/-52.8 232.59+/-162.79 N1=40, N2=6 Fold Change: 2.54 P-value: .00734	X	X
258	512	AI557210	126.32+/-140.31 534.58+/-397.4 N1=40, N2=168 Fold Change: 4.98 P-value: 0	X	X	129.15+/-140.98 364.46+/-223.6 N1=40, N2=31 Fold Change: 3.55 P-value: 0	129.15+/-140.98 306.19+/-192.07 N1=40, N2=10 Fold Change: 2.84 P-value: .00915
259	515	AI560064	X	X	X	885.2+/-306.13 473.3+/-341.89 N1=40, N2=31 Fold Change: 2.17 P-value: 0	885.2+/-306.13 284.56+/-117.13 N1=40, N2=10 Fold Change: 3.2 P-value: .00002

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
260	516	AI560159	X	X	X	249.15+/-159.54 475.18+/-183.53 N1=40, N2=31 Fold Change: 2.08 P-value: 0	249.15+/-159.54 849.92+/-667.24 N1=40, N2=10 Fold Change: 3.13 P-value: .00061
261	517	AI566038	257.62+/-109.32 154.67+/-104.12 N1=39, N2=168 Fold Change: 1.94 P-value: 0	X	X	436.1+/-150.59 302.74+/-153.34 N1=39, N2=31 Fold Change: 1.57 P-value: .00104	X
262	523	AI583942	231.62+/-1223.34 574.26+/-2305.76 N1=40, N2=168 Fold Change: 2.18 P-value: .00076	X	X	237.55+/-1238.75 1788.59+/-4779.29 N1=40, N2=31 Fold Change: 4.69 P-value: .00099	X
263	524	AI587178	X	X	X	X	222.78+/-143.35 88.43+/-75.43 N1=40, N2=10 Fold Change: 2.64 P-value: .00579
264	526	AI589858	296.87+/-162.49 138.95+/-123 N1=39, N2=168 Fold Change: 2.17 P-value: 0	X	X	296.87+/-162.49 143.85+/-108.99 N1=39, N2=31 Fold Change: 2.1 P-value: .00002	296.87+/-162.49 121.61+/-47.86 N1=39, N2=6 Fold Change: 2.31 P-value: .00132
265	527	AI590093	316.95+/-171.55 167.02+/-141.99 N1=40, N2=168 Fold Change: 2.1 P-value: 0	X	X	314.33+/-172.98 149.67+/-84.85 N1=40, N2=31 Fold Change: 2.08 P-value: .00003	314.33+/-172.98 121.07+/-88.54 N1=40, N2=10 Fold Change: 2.91 P-value: .00504
266	529	AI598252	X	X	X	417.54+/-196.25 833.81+/-317.16 N1=39, N2=31 Fold Change: 2.06 P-value: 0	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
267	**530**	**AI601149**	270.5+/-122.37 115.84+/-107.17 N1=40, N2=168 Fold Change: 2.62 P-value: 0	X	X	267.15+/-122.1 101.95+/-53.86 N1=40, N2=31 Fold Change: 2.69 P-value: 0	267.15+/-122.1 55.7+/-20.35 N1=40, N2=10 Fold Change: 4.57 P-value: 0
268	**532**	**AI610837**	2072.69+/-1692.17 724.59+/-659.17 N1=40, N2=168 Fold Change: 2.65 P-value: 0	X	X	2072.69+/-1692.17 544+/-358.27 N1=40, N2=31 Fold Change: 3.17 P-value: 0	2072.69+/-1692.17 319.79+/-159.71 N1=40, N2=10 Fold Change: 4.66 P-value: 0
269	**534**	**AI620381**	X	X	X	X	610.77+/-316.3 1217.36+/-274.04 N1=40, N2=10 Fold Change: 2.16 P-value: 0
270	**535**	**AI624103**	289.59+/-159.89 123.14+/-143.73 N1=39, N2=168 Fold Change: 2.74 P-value: 0	X	289.59+/-159.89 116.4+/-81.91 N1=39, N2=10 Fold Change: 2.65 P-value: .03426	289.59+/-159.89 82.42+/-59.19 N1=39, N2=31 Fold Change: 3.4 P-value: 0	289.59+/-159.89 71.19+/-34.34 N1=39, N2=6 Fold Change: 3.74 P-value: 0
271	**537**	**AI631301**	328.42+/-165.41 126.68+/-74.53 N1=39, N2=168 Fold Change: 2.52 P-value: 0	X	X	328.42+/-165.41 111+/-70.99 N1=39, N2=31 Fold Change: 2.8 P-value: 0	328.42+/-165.41 58.7+/-32.01 N1=39, N2=6 Fold Change: 5.02 P-value: 0
272	**538**	**AI631850**	X	X	X	26.13+/-35.18 224.44+/-595.61 N1=40, N2=31 Fold Change: 2.14 P-value: .00784	X
273	**540**	**AI634852**	X	X	X	278.07+/-162.92 171.54+/-216.03 N1=40, N2=31 Fold Change: 2.18 P-value: .0011	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
274	541	AI635774	212.33+/-93.64 92.03+/-51.47 N1=39, N2=168 Fold Change: 2.39 P-value: 0	X	X	212.33+/-93.64 93.14+/-61.28 N1=39, N2=31 Fold Change: 2.5 P-value: 0	212.33+/-93.64 89.05+/-56.69 N1=39, N2=6 Fold Change: 2.62 P-value: .00169
275	546	AI650514	108.33+/-162.01 321.96+/-278.48 N1=40, N2=168 Fold Change: 3.14 P-value: 0	X	110.57+/-163.5 306.38+/-174.2 N1=40, N2=6 Fold Change: 3.3 P-value: .02515	110.57+/-163.5 495.16+/-349.41 N1=40, N2=31 Fold Change: 5.31 P-value: 0	110.57+/-163.5 380.44+/-266.81 N1=40, N2=10 Fold Change: 3.44 P-value: .01035
276	550	AI651732	X	X	X	X	200.01+/-105.06 67.38+/-39.88 N1=40, N2=10 Fold Change: 3.01 P-value: .00028
277	551	AI652058	X	X	X	X	182.73+/-51.39 384.98+/-89.44 N1=40, N2=10 Fold Change: 2.14 P-value: 0
278	552	AI652459	X	X	X	X	724.8+/-344.86 274.16+/-175.44 N1=40, N2=10 Fold Change: 2.8 P-value: .00159
279	554	AI653487	251.37+/-223.37 44.78+/-81.85 N1=39, N2=168 Fold Change: 3.04 P-value: 0	X	251.37+/-223.37 41.71+/-73.61 N1=39, N2=10 Fold Change: 3.36 P-value: .00441	251.37+/-223.37 30.69+/-76.04 N1=39, N2=31 Fold Change: 3.36 P-value: 0	251.37+/-223.37 4.44+/-69.04 N1=39, N2=6 Fold Change: 4.16 P-value: .00002
280	555	AI654035	227.06+/-388.81 65.4+/-275.63 N1=40, N2=168 Fold Change: 2.9 P-value: .00003	X	X	227.06+/-388.81 56.3+/-242.23 N1=40, N2=31 Fold Change: 3.21 P-value: .0001	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
281	556	AI655499	46.97+/-125.7 313.1+/-881.21 N1=40, N2=168 Fold Change: 2.28 P-value: 0	X	X	47.75+/-127.24 453.25+/-957.09 N1=40, N2=31 Fold Change: 2.89 P-value: .00225	X
282	560	AI656836	X	X	X	X	496.58+/-144.86 242.93+/-91.56 N1=40, N2=10 Fold Change: 2.07 P-value: .00005
283	562	AI658925	545.69+/-343.76 259.08+/-213.04 N1=40, N2=168 Fold Change: 2.3 P-value: 0	X	X	542.56+/-347.67 233.63+/-187.46 N1=40, N2=31 Fold Change: 2.42 P-value: .00001	542.56+/-347.67 164.54+/-115.15 N1=40, N2=10 Fold Change: 3.62 P-value: .00181
284	563	AI658928	230.91+/-89.43 89.62+/-64.08 N1=39, N2=168 Fold Change: 2.76 P-value: 0	X	X	230.91+/-89.43 75.71+/-63.86 N1=39, N2=31 Fold Change: 3.17 P-value: 0	230.91+/-89.43 130.21+/-102.4 N1=39, N2=6 Fold Change: 2.16 P-value: .02073
285	565	AI659418	X	X	X	X	261.02+/-116.11 125.48+/-61.12 N1=40, N2=10 Fold Change: 2.05 P-value: .00057
286	566	AI659533	566.04+/-199.44 260.59+/-219.32 N1=40, N2=168 Fold Change: 2.68 P-value: 0	X	X	563.4+/-201.34 289.88+/-264.96 N1=40, N2=31 Fold Change: 2.58 P-value: 0	563.4+/-201.34 161.05+/-65.87 N1=40, N2=10 Fold Change: 3.49 P-value: 0
287	568	AI659927	X	X	X	X	427.88+/-182.76 161.17+/-86.36 N1=40, N2=10 Fold Change: 2.71 P-value: .00004

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
288	569	AI660245	119.06+/-130.86 277.49+/-246.97 N1=39, N2=168 Fold Change: 2.1 P-value: 0	X	X	X	119.06+/-130.86 357.85+/-302.39 N1=39, N2=6 Fold Change: 2.63 P-value: .01212
289	571	AI668620	X	X	X	1443.34+/-1731.78 1028.64+/-1669.79 N1=40, N2=31 Fold Change: 2.82 P-value: .01542	X
290	574	AI671836	X	X	X	X	112+/-77.42 229.83+/-111.91 N1=40, N2=10 Fold Change: 2.3 P-value: .00034
291	575	AI671984	X	X	X	X	172.75+/-104.93 326.06+/-163.08 N1=40, N2=10 Fold Change: 2.1 P-value: .00523
292	579	AI673539	X	X	X	285.7+/-185.25 643.27+/-468.95 N1=40, N2=31 Fold Change: 2.17 P-value: .00012	X
293	580	AI673735	X	X	X	281.86+/-139.36 128.43+/-98.38 N1=40, N2=31 Fold Change: 2.34 P-value: .00001	X
294	583	AI674603	X	X	X	278.54+/-168.6 119.84+/-49.46 N1=40, N2=31 Fold Change: 2.13 P-value: 0	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
295	584	AI675106	353.92+/-130.58 188.82+/-101.49 N1=39, N2=168 Fold Change: 2.02 P-value: 0	X	X	X	X
296	588	AI680541	516.15+/-202.37 138.66+/-107.52 N1=40, N2=168 Fold Change: 4.19 P-value: 0	X	X	510.08+/-201.29 149.24+/-129.55 N1=40, N2=31 Fold Change: 3.77 P-value: 0	510.08+/-201.29 101.96+/-86.37 N1=40, N2=10 Fold Change: 5.63 P-value: .00001
297	590	AI683036	106.33+/-110.74 328.16+/-267.3 N1=39, N2=168 Fold Change: 2.81 P-value: 0	X	X	106.33+/-110.74 296.92+/-224.37 N1=39, N2=31 Fold Change: 2.63 P-value: 0	X
298	591	AI683911	241.46+/-200.89 35.47+/-57.1 N1=40, N2=168 Fold Change: 4.64 P-value: 0	X	X	241.46+/-200.89 28.41+/-33.49 N1=40, N2=31 Fold Change: 5.05 P-value: 0	241.46+/-200.89 29.45+/-35.37 N1=40, N2=10 Fold Change: 5.29 P-value: 0
299	592	AI684457	96.99+/-74.31 233.36+/-405.3 N1=40, N2=168 Fold Change: 2 P-value: .00001	X	X	X	X
300	593	AI686114	375.54+/-271.13 158.93+/-158.15 N1=40, N2=168 Fold Change: 2.67 P-value: 0	X	X	374.48+/-274.59 155.96+/-124.29 N1=40, N2=31 Fold Change: 2.4 P-value: .00006	X
301	594	AI686316	255.25+/-97.58 102.19+/-93.67 N1=39, N2=168 Fold Change: 2.55 P-value: 0	X	255.25+/-97.58 120.04+/-93.28 N1=39, N2=10 Fold Change: 2.52 P-value: .0397	255.25+/-97.58 79.78+/-67.6 N1=39, N2=31 Fold Change: 2.99 P-value: 0	255.25+/-97.58 51.42+/-78.59 N1=39, N2=6 Fold Change: 3.34 P-value: .00001

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
302	595	AI689747	229.57+/-81.34 113.53+/-98.71 N1=39, N2=168 Fold Change: 2.2 P-value: 0	X	X	229.57+/-81.34 120.42+/-76.86 N1=39, N2=31 Fold Change: 2.07 P-value: 0	229.57+/-81.34 74.4+/-34.38 N1=39, N2=6 Fold Change: 2.9 P-value: 0
303	597	AI691077	201.9+/-110.51 84.62+/-106.12 N1=40, N2=168 Fold Change: 2.35 P-value: 0	X	X	X	X
304	599	AI692687	X	X	X	X	215.65+/-82.22 106.33+/-67.45 N1=39, N2=6 Fold Change: 2.27 P-value: .00376
305	603	AI693690	X	X	X	X	187.55+/-153.71 419.84+/-166.89 N1=40, N2=10 Fold Change: 2.84 P-value: .00002
306	604	AI694059	256.63+/-189.71 63.49+/-68.69 N1=39, N2=168 Fold Change: 3.4 P-value: 0	X	X	256.63+/-189.71 45.9+/-74.24 N1=39, N2=31 Fold Change: 3.8 P-value: 0	256.63+/-189.71 24.83+/-23.88 N1=39, N2=6 Fold Change: 5.35 P-value: 0
307	606	AI695684	X	X	X	X	284.08+/-85.43 138.19+/-31.83 N1=40, N2=10 Fold Change: 2.01 P-value: 0
308	608	AI698134	801.15+/-394.52 295.3+/-157.04 N1=40, N2=168 Fold Change: 2.66 P-value: 0	X	803.86+/-399.3 305.4+/-156.08 N1=40, N2=6 Fold Change: 2.52 P-value: .00483	803.86+/-399.3 238.5+/-98.66 N1=40, N2=31 Fold Change: 3.16 P-value: 0	803.86+/-399.3 290.26+/-225.95 N1=40, N2=10 Fold Change: 3.23 P-value: .00182

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
309	610	AI700484	404.49+/-304.86 149.98+/-93.82 N1=40, N2=168 Fold Change: 2.59 P-value: 0	X	404.49+/-304.86 151.52+/-60.91 N1=40, N2=6 Fold Change: 2.49 P-value: .00796	404.49+/-304.86 139.3+/-55.78 N1=40, N2=31 Fold Change: 2.66 P-value: 0	404.49+/-304.86 132.26+/-50.46 N1=40, N2=10 Fold Change: 2.75 P-value: 0
310	612	AI701034	X	X	X	X	215.78+/-96.65 101.91+/-38.36 N1=40, N2=10 Fold Change: 2.03 P-value: .00018
311	613	AI703441	X	X	X	166.32+/-110.39 348.27+/-255.22 N1=40, N2=31 Fold Change: 2 P-value: .00052	166.32+/-110.39 332.43+/-137.78 N1=40, N2=10 Fold Change: 2.31 P-value: .00003
312	614	AI703451	X	X	X	58.72+/-154.11 479.31+/-977.92 N1=40, N2=31 Fold Change: 3.05 P-value: .00313	X
313	615	AI707589	446.78+/-668.95 359.77+/-1435.2 N1=40, N2=168 Fold Change: 2.73 P-value: .00099	X	X	414.9+/-646.18 236.79+/-693.96 N1=40, N2=31 Fold Change: 2.49 P-value: .01893	414.9+/-646.18 -8.82+/-71.63 N1=40, N2=10 Fold Change: 4.36 P-value: .00006
314	617	AI720763	X	X	X	X	216.2+/-123.53 94.49+/-39.1 N1=40, N2=10 Fold Change: 2.05 P-value: .00026
315	618	AI732274	926.55+/-985.51 133.4+/-273.85 N1=40, N2=168 Fold Change: 7.17 P-value: 0	X	947.08+/-989.69 92.83+/-139.88 N1=40, N2=6 Fold Change: 8.37 P-value: .00451	947.08+/-989.69 17.45+/-85.58 N1=40, N2=31 Fold Change: 13.2 P-value: 0	947.08+/-989.69 25.59+/-138.38 N1=40, N2=10 Fold Change: 14.18 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
316	619	AI733679	319.55+/-589.9 41.3+/-61.11 N1=40, N2=168 Fold Change: 3.96 P-value: 0	X	325.9+/-596.22 26.3+/-20.79 N1=40, N2=6 Fold Change: 4.56 P-value: .00001	325.9+/-596.22 23.3+/-13.87 N1=40, N2=31 Fold Change: 5.05 P-value: 0	325.9+/-596.22 22.92+/-14.21 N1=40, N2=10 Fold Change: 5.39 P-value: 0
317	621	AI740483	X	X	X	X	519.7+/-165.79 245.74+/-94.64 N1=39, N2=6 Fold Change: 2.11 P-value: .00011
318	622	AI740516	23.68+/-49.95 230.26+/-254.07 N1=40, N2=168 Fold Change: 5.25 P-value: 0	X	X	24.14+/-50.52 211.05+/-266.38 N1=40, N2=31 Fold Change: 4.63 P-value: 0	X
319	623	AI740621	231.84+/-247.13 51.4+/-63.67 N1=40, N2=168 Fold Change: 2.99 P-value: 0	X	X	231.84+/-247.13 55.89+/-78.15 N1=40, N2=31 Fold Change: 2.92 P-value: .00006	231.84+/-247.13 58.59+/-71.76 N1=40, N2=10 Fold Change: 2.89 P-value: .00645
320	624	AI741026	324.97+/-140.14 152.41+/-75.46 N1=40, N2=168 Fold Change: 2.1 P-value: 0	X	X	321.67+/-140.4 156.42+/-93.26 N1=40, N2=31 Fold Change: 2.06 P-value: 0	X
321	627	AI742002	109.12+/-131.8 356.63+/-240.05 N1=40, N2=168 Fold Change: 3.82 P-value: 0	X	111.78+/-132.43 392.25+/-219.22 N1=40, N2=6 Fold Change: 4.18 P-value: .00524	111.78+/-132.43 395.11+/-278.86 N1=40, N2=31 Fold Change: 3.97 P-value: 0	111.78+/-132.43 430.05+/-236.92 N1=40, N2=10 Fold Change: 4.87 P-value: 0
322	628	AI742057	200.43+/-229.58 445.89+/-295.68 N1=40, N2=168 Fold Change: 2.37 P-value: 0	X	X	203.47+/-231.77 460.52+/-275.2 N1=40, N2=31 Fold Change: 2.6 P-value: 0	203.47+/-231.77 448.38+/-232.46 N1=40, N2=10 Fold Change: 2.46 P-value: .00303

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
323	629	AI742239	160.34+/-196.79 321.12+/-260.74 N1=40, N2=168 Fold Change: 2.24 P-value: .00004	X	X	159.76+/-199.32 420.92+/-297.86 N1=40, N2=31 Fold Change: 3.17 P-value: .00002	X
324	631	AI742490	608.25+/-253.14 244.8+/-205.92 N1=40, N2=168 Fold Change: 2.99 P-value: 0	X	X	601.57+/-252.84 202.34+/-107.23 N1=40, N2=31 Fold Change: 3.01 P-value: 0	601.57+/-252.84 135.78+/-110.24 N1=40, N2=10 Fold Change: 5.03 P-value: .00005
325	632	AI742521	213.11+/-232.57 35.67+/-56.27 N1=40, N2=168 Fold Change: 3.92 P-value: 0	X	215.93+/-234.91 60.9+/-90.73 N1=40, N2=6 Fold Change: 3.31 P-value: .02617	215.93+/-234.91 35.9+/-49 N1=40, N2=31 Fold Change: 3.94 P-value: 0	215.93+/-234.91 21.54+/-22.52 N1=40, N2=10 Fold Change: 4.49 P-value: 0
326	635	AI743671	578.21+/-315.16 225.87+/-183.42 N1=40, N2=168 Fold Change: 2.79 P-value: 0	X	X	582.82+/-317.91 172.55+/-151.01 N1=40, N2=31 Fold Change: 3.82 P-value: 0	582.82+/-317.91 150.6+/-109.83 N1=40, N2=10 Fold Change: 3.98 P-value: .0009
327	636	AI743715	320.58+/-241.61 99.04+/-151.07 N1=40, N2=168 Fold Change: 3.54 P-value: 0	X	X	312.02+/-238.55 78.92+/-130.98 N1=40, N2=31 Fold Change: 4.04 P-value: 0	312.02+/-238.55 17.92+/-64.11 N1=40, N2=10 Fold Change: 6.18 P-value: .00001
328	637	AI743925	665.72+/-305.69 344.09+/-309.12 N1=40, N2=168 Fold Change: 2.33 P-value: 0	X	X	X	X
329	639	AI745624	X	X	X	210.12+/-81.11 116.93+/-65.22 N1=39, N2=31 Fold Change: 1.89 P-value: 0	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
330	640	AI750575	702.71+/-253.03 412.71+/-328.09 N1=40, N2=168 Fold Change: 2.14 P-value: 0	X	X	697.86+/-254.44 377.83+/-298.25 N1=40, N2=31 Fold Change: 2.36 P-value: .00005	697.86+/-254.44 275.21+/-286.22 N1=40, N2=10 Fold Change: 3.89 P-value: .00699
331	641	AI751438	141.85+/-187.15 658.02+/-724.54 N1=40, N2=168 Fold Change: 4.71 P-value: 0	X	X	144.67+/-188.73 466.36+/-471.12 N1=40, N2=31 Fold Change: 3.51 P-value: 0	144.67+/-188.73 306.05+/-201.86 N1=40, N2=10 Fold Change: 2.79 P-value: .00492
332	642	AI752682	375.26+/-189.87 160.22+/-155.84 N1=40, N2=168 Fold Change: 3.01 P-value: 0	X	X	369.82+/-189.17 148.94+/-124.57 N1=40, N2=31 Fold Change: 2.85 P-value: .00001	369.82+/-189.17 76.67+/-82.11 N1=40, N2=10 Fold Change: 5.81 P-value: .00014
333	643	AI758223	836.07+/-657.44 153.81+/-456.44 N1=40, N2=168 Fold Change: 9.32 P-value: 0	X	833.52+/-665.83 215.9+/-314.77 N1=40, N2=6 Fold Change: 6.2 P-value: .02859	833.52+/-665.83 164.76+/-581.67 N1=40, N2=31 Fold Change: 10.99 P-value: 0	833.52+/-665.83 52.12+/-64.89 N1=40, N2=10 Fold Change: 14.24 P-value: 0
334	644	AI758408	X	X	X	X	383.82+/-126.82 188.25+/-213.28 N1=40, N2=10 Fold Change: 3.58 P-value: .01039
335	645	AI760319	208.69+/-65.34 105.79+/-40.89 N1=39, N2=168 Fold Change: 2 P-value: 0	X	208.69+/-65.34 102.62+/-62.32 N1=39, N2=10 Fold Change: 2.02 P-value: .01579	208.69+/-65.34 102.48+/-38.82 N1=39, N2=31 Fold Change: 2.07 P-value: 0	208.69+/-65.34 104.41+/-52.84 N1=39, N2=6 Fold Change: 2.13 P-value: .00136
336	646	AI760370	X	X	X	691.21+/-512.28 259.02+/-226.94 N1=40, N2=31 Fold Change: 2.3 P-value: .00272	691.21+/-512.28 142.47+/-133.11 N1=40, N2=10 Fold Change: 4.03 P-value: .00082

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
337	648	AI760589	X	X	X	81.29+/-140.48 214.53+/-216.44 N1=40, N2=31 Fold Change: 3.26 P-value: 0	X
338	649	AI761241	891.41+/-331.82 417.19+/-273.72 N1=40, N2=168 Fold Change: 2.32 P-value: 0	X	X	883.3+/-332.12 352.83+/-245.83 N1=40, N2=31 Fold Change: 2.7 P-value: 0	883.3+/-332.12 238.36+/-101.2 N1=40, N2=10 Fold Change: 3.83 P-value: .00005
339	650	AI761274	346.01+/-181.77 114.5+/-91.9 N1=40, N2=168 Fold Change: 3.44 P-value: 0	X	X	342.36+/-182.65 121.75+/-92.05 N1=40, N2=31 Fold Change: 3.23 P-value: 0	342.36+/-182.65 77.48+/-76.11 N1=40, N2=10 Fold Change: 4.73 P-value: .00028
340	651	AI761782	X	X	X	X	41.02+/-103.08 282.44+/-98.22 N1=39, N2=6 Fold Change: 6.26 P-value: 0
341	652	AI761844	284.64+/-141.48 117.61+/-150.43 N1=40, N2=168 Fold Change: 2.8 P-value: 0	X	X	278.83+/-138.41 132.4+/-302.8 N1=40, N2=31 Fold Change: 3.35 P-value: 0	278.83+/-138.41 94.71+/-60.55 N1=40, N2=10 Fold Change: 3.05 P-value: .0007
342	654	AI763298	247.25+/-99.93 113.86+/-100.53 N1=40, N2=168 Fold Change: 2.6 P-value: 0	X	X	242.06+/-95.62 148.77+/-173.93 N1=40, N2=31 Fold Change: 2.29 P-value: .00002	242.06+/-95.62 84.64+/-67.22 N1=40, N2=10 Fold Change: 3.32 P-value: .00045
343	655	AI766029	265.74+/-522.75 15.92+/-35.83 N1=40, N2=168 Fold Change: 3.94 P-value: 0	X	271.74+/-528.19 11.19+/-13.38 N1=40, N2=6 Fold Change: 4.33 P-value: 0	271.74+/-528.19 4.73+/-8.61 N1=40, N2=31 Fold Change: 4.64 P-value: 0	271.74+/-528.19 8.83+/-25.01 N1=40, N2=10 Fold Change: 4.09 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
344	659	AI768777	X	X	X	X	263.99+/-143.63 686.1+/-326.01 N1=40, N2=10 Fold Change: 2.67 P-value: .00011
345	661	AI769559	X	X	X	213.16+/-92.6 101.34+/-76.51 N1=39, N2=31 Fold Change: 2.13 P-value: 0	X
346	662	AI770080	450.33+/-335.5 166.16+/-190.29 N1=40, N2=168 Fold Change: 2.79 P-value: 0	X	X	453.96+/-339.09 129.2+/-107.13 N1=40, N2=31 Fold Change: 3.2 P-value: 0	453.96+/-339.09 94.56+/-93.08 N1=40, N2=10 Fold Change: 4.55 P-value: .00046
347	663	AI783490	767.15+/-947.17 1513.38+/-2167.1 N1=40, N2=168 Fold Change: 2.14 P-value: .00537	X	X	X	X
348	665	AI791632	255.06+/-150.68 122.84+/-86.83 N1=40, N2=168 Fold Change: 2.22 P-value: 0	X	X	X	255.06+/-150.68 96.82+/-63.86 N1=40, N2=10 Fold Change: 2.58 P-value: .00084
349	667	AI792405	X	X	X	93.82+/-112.78 202.01+/-224.89 N1=40, N2=31 Fold Change: 2.02 P-value: .00448	X
350	669	AI792817	112.38+/-143.52 558.02+/-937.45 N1=40, N2=168 Fold Change: 3.33 P-value: 0	X	X	112.38+/-143.52 510.79+/-557.67 N1=40, N2=31 Fold Change: 3.97 P-value: 0	112.38+/-143.52 849.79+/-711.76 N1=40, N2=10 Fold Change: 7.3 P-value: .00101

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
351	670	AI795953	407.3+/-278.56 146.44+/-111.32 N1=39, N2=168 Fold Change: 2.62 P-value: 0	X	407.3+/-278.56 173.14+/-117.81 N1=39, N2=10 Fold Change: 2.32 P-value: .03224	407.3+/-278.56 122.61+/-57.78 N1=39, N2=31 Fold Change: 2.89 P-value: 0	407.3+/-278.56 137.64+/-123.78 N1=39, N2=6 Fold Change: 3.16 P-value: .00069
352	671	AI796083	X	X	114.7+/-66.6 207.1+/-77.72 N1=40, N2=6 Fold Change: 2.06 P-value: .00108	X	X
353	672	AI796210	300.25+/-171.19 136.42+/-160.54 N1=39, N2=168 Fold Change: 2.45 P-value: 0	X	X	300.25+/-171.19 142.27+/-164.88 N1=39, N2=31 Fold Change: 2.36 P-value: 0	300.25+/-171.19 68.23+/-32.91 N1=39, N2=6 Fold Change: 3.93 P-value: 0
354	673	AI797063	217.39+/-201.68 181.18+/-462.43 N1=40, N2=168 Fold Change: 2.2 P-value: .00014	X	X	220.19+/-203.53 161.62+/-454.65 N1=40, N2=31 Fold Change: 3.09 P-value: .00028	220.19+/-203.53 58.77+/-92.21 N1=40, N2=10 Fold Change: 3.3 P-value: .00535
355	674	AI797276	270.66+/-135.07 91.42+/-65.13 N1=40, N2=168 Fold Change: 3.1 P-value: 0	X	271.48+/-136.73 110.91+/-50.09 N1=40, N2=6 Fold Change: 2.28 P-value: .00368	271.48+/-136.73 84.22+/-53.14 N1=40, N2=31 Fold Change: 3.2 P-value: 0	271.48+/-136.73 51.53+/-37.65 N1=40, N2=10 Fold Change: 5.08 P-value: 0
356	675	AI797788	X	X	X	X	268.73+/-161.42 121.99+/-102 N1=40, N2=10 Fold Change: 2.27 P-value: .00827
357	676	AI798144	74.39+/-112.61 243.81+/-208.55 N1=39, N2=168 Fold Change: 2.13 P-value: 0	X	X	X	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
358	678	AI799784	599.82+/-379.39 67.15+/-81.53 N1=40, N2=168 Fold Change: 9.18 P-value: 0	X	603.99+/-383.42 148.43+/-186.96 N1=40, N2=6 Fold Change: 5.77 P-value: .01759	603.99+/-383.42 63.08+/-91.29 N1=40, N2=31 Fold Change: 10.41 P-value: 0	603.99+/-383.42 38.2+/-47.49 N1=40, N2=10 Fold Change: 14.19 P-value: 0
359	681	AI801545	X	X	X	X	107.72+/-63.11 240.16+/-135.66 N1=40, N2=10 Fold Change: 2.33 P-value: .00036
360	682	AI803208	X	X	X	X	358.64+/-152.22 196.65+/-140.61 N1=39, N2=6 Fold Change: 2.05 P-value: .01446
361	683	AI803648	107.03+/-109.9 295.41+/-304.62 N1=39, N2=168 Fold Change: 2.31 P-value: 0	X	X	X	X
362	684	AI804054	307.23+/-232.94 92.54+/-103.69 N1=40, N2=168 Fold Change: 3.71 P-value: 0	X	X	302.97+/-234.41 73.14+/-50.57 N1=40, N2=31 Fold Change: 3.81 P-value: 0	302.97+/-234.41 43.17+/-28.15 N1=40, N2=10 Fold Change: 5.95 P-value: 0
363	686	AI806221	206.98+/-125.27 57.8+/-39.92 N1=39, N2=168 Fold Change: 3.4 P-value: 0	X	206.98+/-125.27 64.87+/-57.18 N1=39, N2=10 Fold Change: 2.98 P-value: .00675	206.98+/-125.27 49.38+/-39.25 N1=39, N2=31 Fold Change: 3.82 P-value: 0	206.98+/-125.27 31.17+/-27.12 N1=39, N2=6 Fold Change: 5.54 P-value: 0
364	687	AI806324	214.04+/-130.5 64.16+/-76.08 N1=40, N2=168 Fold Change: 3.61 P-value: 0	X	X	211.46+/-131.17 48.58+/-64.25 N1=40, N2=31 Fold Change: 4.36 P-value: 0	211.46+/-131.17 21.48+/-26.9 N1=40, N2=10 Fold Change: 6.44 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
365	690	AI809925	X	X	X	283.79+/-467.54 95.99+/-60.68 N1=40, N2=31 Fold Change: 2.37 P-value: .00001	283.79+/-467.54 72.84+/-38.61 N1=40, N2=10 Fold Change: 3.03 P-value: .00019
366	691	AI809953	383.3+/-186.88 78.06+/-108.22 N1=40, N2=168 Fold Change: 5.91 P-value: 0	X	X	383.43+/-189.32 59.3+/-98.99 N1=40, N2=31 Fold Change: 7.01 P-value: 0	383.43+/-189.32 19.05+/-40.62 N1=40, N2=10 Fold Change: 10.5 P-value: 0
367	692	AI810042	X	X	X	X	494.45+/-173.8 211.09+/-46.06 N1=40, N2=10 Fold Change: 2.24 P-value: 0
368	693	AI810266	68.69+/-105.28 955.73+/-1984.55 N1=40, N2=168 Fold Change: 6.41 P-value: 0	X	68.88+/-106.64 1044.03+/-865.49 N1=40, N2=6 Fold Change: 16.18 P-value: .00033	68.88+/-106.64 1634.45+/-2196.2 N1=40, N2=31 Fold Change: 13.8 P-value: 0	68.88+/-106.64 521.04+/-362.47 N1=40, N2=10 Fold Change: 9.22 P-value: 0
369	694	AI810764	X	X	X	202.16+/-159.83 408.84+/-303.87 N1=40, N2=31 Fold Change: 2.01 P-value: .00293	X
370	700	AI816806	551.09+/-313.71 267.19+/-176.02 N1=40, N2=168 Fold Change: 2.1 P-value: 0	X	X	560.99+/-311.41 242.91+/-135.88 N1=40, N2=31 Fold Change: 2.3 P-value: 0	560.99+/-311.41 221.89+/-110.66 N1=40, N2=10 Fold Change: 2.4 P-value: .00018
371	701	AI816835	360.85+/-289.77 146.43+/-155.9 N1=40, N2=168 Fold Change: 2.82 P-value: 0	X	X	360.85+/-289.77 158.38+/-181.37 N1=40, N2=31 Fold Change: 2.55 P-value: .00002	360.85+/-289.77 80.71+/-87.22 N1=40, N2=10 Fold Change: 4.99 P-value: .00046

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
372	702	AI817448	X	X	X	X	241.5+/-87.57 116.59+/-51.83 N1=40, N2=10 Fold Change: 2.2 P-value: .003
373	703	AI817698	X	X	X	879.11+/-582.6 519.31+/-493.58 N1=40, N2=31 Fold Change: 2.38 P-value: .0048	X
374	706	AI818579	396.29+/-225.56 181.53+/-192.42 N1=40, N2=168 Fold Change: 2.49 P-value: 0	X	X	394.08+/-228.07 173.3+/-120.25 N1=40, N2=31 Fold Change: 2.39 P-value: .00004	X
375	707	AI819198	X	X	X	24.28+/-46.39 341.95+/-719 N1=40, N2=31 Fold Change: 2.75 P-value: .00243	X
376	708	AI819340	60.25+/-126.35 301.57+/-342.95 N1=40, N2=168 Fold Change: 3.51 P-value: 0	X	63.25+/-126.56 247.5+/-201.27 N1=40, N2=6 Fold Change: 3.53 P-value: .04505	63.25+/-126.56 468.97+/-447.94 N1=40, N2=31 Fold Change: 5.82 P-value: 0	63.25+/-126.56 450.47+/-509.91 N1=40, N2=10 Fold Change: 4.85 P-value: .00541
377	709	AI820661	-117.72+/-96.27 255.76+/-788.64 N1=40, N2=168 Fold Change: 2.95 P-value: 0	X	X	X	X
378	711	AI821432	X	X	X	349.15+/-245.88 114.84+/-86.63 N1=40, N2=31 Fold Change: 2.66 P-value: .00004	349.15+/-245.88 55.83+/-64.32 N1=40, N2=10 Fold Change: 5.96 P-value: .00004

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
379	712	AI821472	524.32+/-685.96 227.66+/-1932.77 N1=40, N2=168 Fold Change: 5.78 P-value: 0	X	519.11+/-694.13 10.64+/-179.34 N1=40, N2=6 Fold Change: 4.41 P-value: .02894	519.11+/-694.13 83.31+/-629.25 N1=40, N2=31 Fold Change: 5.76 P-value: 0	X
380	713	AI823572	231.34+/-193.19 124.55+/-179.13 N1=40, N2=168 Fold Change: 2.37 P-value: 0	X	X	232.21+/-195.63 80.48+/-58.66 N1=40, N2=31 Fold Change: 2.82 P-value: 0	X
381	714	AI823649	88.12+/-78.99 225.47+/-213.09 N1=39, N2=168 Fold Change: 2.16 P-value: 0	X	X	88.12+/-78.99 223.88+/-174.27 N1=39, N2=31 Fold Change: 2.31 P-value: 0	88.12+/-78.99 239.23+/-237.92 N1=39, N2=6 Fold Change: 2.2 P-value: .01309
382	720	AI825877	X	X	X	418.53+/-162.52 174.35+/-58.42 N1=40, N2=31 Fold Change: 2.28 P-value: 0	418.53+/-162.52 183.59+/-84.31 N1=40, N2=10 Fold Change: 2.23 P-value: .00011
383	722	AI826437	44.87+/-117.62 241.17+/-525.8 N1=40, N2=168 Fold Change: 2.29 P-value: 0	X	X	45.86+/-118.99 347.56+/-551.29 N1=40, N2=31 Fold Change: 3.07 P-value: .00134	X
384	723	AI827230	711.88+/-268 325.69+/-167.35 N1=40, N2=168 Fold Change: 2.22 P-value: 0	X	X	708.38+/-270.57 266.08+/-114.65 N1=40, N2=31 Fold Change: 2.67 P-value: 0	708.38+/-270.57 273.56+/-97.64 N1=40, N2=10 Fold Change: 2.5 P-value: 0
385	724	AI827248	X	X	X	X	1009.54+/-892.35 424.88+/-561.45 N1=40, N2=10 Fold Change: 3.8 P-value: .0309

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
386	725	AI828075	X	X	X	X	55.74+/-25.88 208.73+/-146.52 N1=40, N2=10 Fold Change: 3.44 P-value: .0001
387	730	AI829520	78.95+/-63.55 221.75+/-308.11 N1=39, N2=168 Fold Change: 2.05 P-value: 0	X	X	X	X
388	733	AI833102	X	X	X	X	152.23+/-73.43 301.22+/-134.13 N1=40, N2=10 Fold Change: 2.05 P-value: .00005
389	734	AI857788	X	X	X	X	201.77+/-88.15 79.71+/-43.65 N1=40, N2=10 Fold Change: 2.61 P-value: .00082
390	735	AI857856	X	X	X	157.81+/-89.37 341.48+/-151.28 N1=39, N2=31 Fold Change: 2.22 P-value: 0	157.81+/-89.37 329.17+/-128.25 N1=39, N2=6 Fold Change: 2.15 P-value: .00013
391	739	AI859620	47.7+/-100.9 335.29+/-308.39 N1=39, N2=168 Fold Change: 4.1 P-value: 0	X	X	47.7+/-100.9 292.66+/-218.11 N1=39, N2=31 Fold Change: 4.09 P-value: 0	47.7+/-100.9 289.43+/-181.71 N1=39, N2=6 Fold Change: 3.84 P-value: .00203
392	740	AI860012	X	X	X	91.22+/-72.75 226.82+/-105.84 N1=39, N2=31 Fold Change: 2.64 P-value: 0	91.22+/-72.75 232.58+/-120.25 N1=39, N2=6 Fold Change: 2.58 P-value: .00185

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
393	742	AI860651	X	X	X	183.59+/-123.14 449.58+/-384.81 N1=40, N2=31 Fold Change: 2.2 P-value: 0	X
394	743	AI863166	X	X	225.98+/-111.31 101.21+/-69.32 N1=39, N2=10 Fold Change: 2.4 P-value: .0473	X	X
395	747	AI864898	406.1+/-256.59 54.76+/-81.97 N1=40, N2=168 Fold Change: 8.17 P-value: 0	X	X	401.86+/-258.51 39.21+/-56.87 N1=40, N2=31 Fold Change: 9.5 P-value: 0	401.86+/-258.51 31.77+/-56.32 N1=40, N2=10 Fold Change: 10.87 P-value: 0
396	748	AI868289	X	X	X	386.08+/-242.58 184.36+/-111.4 N1=40, N2=31 Fold Change: 2.22 P-value: .00003	386.08+/-242.58 156.1+/-103.22 N1=40, N2=10 Fold Change: 2.54 P-value: .00207
397	750	AI871044	777.08+/-499.12 185.08+/-242.68 N1=40, N2=168 Fold Change: 4.86 P-value: 0	X	X	766.39+/-500.99 180.1+/-276.48 N1=40, N2=31 Fold Change: 5.2 P-value: 0	766.39+/-500.99 112.03+/-106.51 N1=40, N2=10 Fold Change: 6.31 P-value: 0
398	751	AI872267	267.23+/-203.1 574.94+/-319.02 N1=40, N2=168 Fold Change: 2.41 P-value: 0	X	X	267.23+/-203.1 557.03+/-278.09 N1=40, N2=31 Fold Change: 2.36 P-value: .00001	267.23+/-203.1 504.87+/-295.04 N1=40, N2=10 Fold Change: 2.17 P-value: .00277
399	753	AI885164	X	X	X	X	99.32+/-89.64 276.5+/-111.42 N1=40, N2=10 Fold Change: 2.94 P-value: .00002

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
400	**754**	**AI885498**	220.94+/-153.32 574.07+/-702.09 N1=40, N2=168 Fold Change: 2.02 P-value: .00005	X	X	X	X
401	**755**	**AI885781**	X	X	X	219.35+/-109.49 556.06+/-397.8 N1=40, N2=31 Fold Change: 2.14 P-value: .00015	219.35+/-109.49 582.43+/-483.5 N1=40, N2=10 Fold Change: 2.47 P-value: .00109
402	**757**	**AI887362**	X	X	X	817.12+/-289.64 355.42+/-140.94 N1=40, N2=31 Fold Change: 2.26 P-value: 0	817.12+/-289.64 243.89+/-105.11 N1=40, N2=10 Fold Change: 3.29 P-value: 0
403	**758**	**AI888322**	X	X	X	319.22+/-320.74 161.88+/-221.65 N1=40, N2=31 Fold Change: 2.73 P-value: .00024	319.22+/-320.74 108.01+/-133 N1=40, N2=10 Fold Change: 3.9 P-value: .00657
404	**761**	**AI889178**	X	X	372.23+/-146.77 183.45+/-70.01 N1=39, N2=10 Fold Change: 2.03 P-value: .00518	372.23+/-146.77 196.21+/-126.54 N1=39, N2=31 Fold Change: 2.04 P-value: 0	372.23+/-146.77 194.59+/-97.59 N1=39, N2=6 Fold Change: 2.03 P-value: .00236
405	**762**	**AI889959**	X	X	X	140.79+/-151.42 298.84+/-296.55 N1=40, N2=31 Fold Change: 2.11 P-value: .00028	140.79+/-151.42 319.25+/-177.44 N1=40, N2=10 Fold Change: 2.62 P-value: .00302
406	**763**	**AI890418**	218.25+/-140.58 37.18+/-39.2 N1=39, N2=168 Fold Change: 3.82 P-value: 0	X	218.25+/-140.58 76.35+/-66.16 N1=39, N2=10 Fold Change: 3.02 P-value: .02078	218.25+/-140.58 35.49+/-32.04 N1=39, N2=31 Fold Change: 3.92 P-value: 0	218.25+/-140.58 26.22+/-48 N1=39, N2=6 Fold Change: 4.12 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
407	764	AI890488	X	X	X	X	498.18+/-173.26 235.59+/-100.47 N1=40, N2=10 Fold Change: 2.19 P-value: .00095
408	769	AI912772	X	X	X	X	124.98+/-38.73 344.88+/-151.12 N1=40, N2=10 Fold Change: 2.65 P-value: .00005
409	772	AI916544	150.68+/-161.18 440.12+/-478.52 N1=40, N2=168 Fold Change: 2.97 P-value: 0	X	X	151.27+/-163.24 548.66+/-436.19 N1=40, N2=31 Fold Change: 3.81 P-value: 0	151.27+/-163.24 636.35+/-560.17 N1=40, N2=10 Fold Change: 3.69 P-value: .01086
410	775	AI917901	591.38+/-804.54 76.3+/-209.26 N1=40, N2=168 Fold Change: 5.07 P-value: 0	X	601.53+/-812.45 57.95+/-67.95 N1=40, N2=6 Fold Change: 4.77 P-value: .00228	601.53+/-812.45 32.64+/-44.74 N1=40, N2=31 Fold Change: 6.97 P-value: 0	601.53+/-812.45 15.05+/-18.69 N1=40, N2=10 Fold Change: 9.62 P-value: 0
411	776	AI921685	102.15+/-191.42 374.73+/-772.23 N1=40, N2=168 Fold Change: 2.03 P-value: .0025	X	X	104.01+/-193.56 633.55+/-1087.03 N1=40, N2=31 Fold Change: 3.3 P-value: .00274	X
412	777	AI922892	X	X	X	203.33+/-90.32 481.16+/-300.69 N1=39, N2=31 Fold Change: 2.13 P-value: 0	203.33+/-90.32 498.39+/-402.89 N1=39, N2=6 Fold Change: 2.02 P-value: .02385
413	778	AI923108	X	X	X	245.08+/-135.84 576.66+/-441.15 N1=40, N2=31 Fold Change: 2.16 P-value: 0	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
414	779	AI924028	X	X	X	X	426.33+/-126.02 190+/-63.01 N1=40, N2=10 Fold Change: 2.25 P-value: .00002
415	780	AI924465	448.27+/-478.27 123.26+/-122.11 N1=40, N2=168 Fold Change: 3.18 P-value: 0	X	448.27+/-478.27 110.32+/-53.45 N1=40, N2=6 Fold Change: 2.73 P-value: .00317	448.27+/-478.27 104.34+/-104.06 N1=40, N2=31 Fold Change: 3.88 P-value: 0	448.27+/-478.27 46.51+/-27.28 N1=40, N2=10 Fold Change: 6.5 P-value: 0
416	781	AI924794	X	X	X	132.27+/-116.84 324.59+/-170.2 N1=39, N2=31 Fold Change: 2.6 P-value: 0	132.27+/-116.84 321.46+/-186.7 N1=39, N2=6 Fold Change: 2.5 P-value: .0029
417	782	AI927695	X	X	X	X	624.33+/-219.53 287.2+/-131.6 N1=40, N2=10 Fold Change: 2.22 P-value: .00029
418	784	AI928296	X	X	X	X	146.02+/-113.56 281.82+/-97.95 N1=40, N2=10 Fold Change: 2.05 P-value: .00016
419	785	AI928393	302.49+/-122.77 166.83+/-119.33 N1=40, N2=168 Fold Change: 2.03 P-value: 0	X	X	297.26+/-119.77 142.57+/-77.64 N1=40, N2=31 Fold Change: 2.17 P-value: 0	297.26+/-119.77 130.31+/-96.66 N1=40, N2=10 Fold Change: 2.67 P-value: .0034
420	787	AI934361	215.99+/-241.37 49.3+/-62.57 N1=40, N2=168 Fold Change: 3.48 P-value: 0	X	220.01+/-243.16 47.28+/-26.36 N1=40, N2=6 Fold Change: 3.18 P-value: .00079	220.01+/-243.16 33.19+/-18.11 N1=40, N2=31 Fold Change: 4.31 P-value: 0	220.01+/-243.16 32.04+/-24.58 N1=40, N2=10 Fold Change: 4.29 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
421	788	AI934407	X	X	X	X	168.61+/-198.83 377.54+/-147.2 N1=40, N2=10 Fold Change: 2.61 P-value: .00001
422	792	AI935915	26.52+/-106.71 267.11+/-334.72 N1=40, N2=168 Fold Change: 4.41 P-value: 0	X	X	28.01+/-107.68 364.49+/-370.15 N1=40, N2=31 Fold Change: 6.74 P-value: 0	28.01+/-107.68 510.1+/-498.57 N1=40, N2=10 Fold Change: 8.29 P-value: .00153
423	793	AI936699	X	X	X	769.05+/-392.56 344.85+/-187.03 N1=40, N2=31 Fold Change: 2.04 P-value: .00007	769.05+/-392.56 208.46+/-65.42 N1=40, N2=10 Fold Change: 3.07 P-value: 0
424	794	AI936823	X	X	X	X	109.06+/-86.01 210.69+/-119.04 N1=40, N2=10 Fold Change: 2.33 P-value: .00059
425	795	AI937060	73.53+/-63.87 221.63+/-200.57 N1=39, N2=168 Fold Change: 2.37 P-value: 0	X	X	73.53+/-63.87 275.58+/-253.28 N1=39, N2=31 Fold Change: 2.86 P-value: 0	73.53+/-63.87 293.86+/-212.3 N1=39, N2=6 Fold Change: 3.17 P-value: .00776
426	796	AI937365	458.68+/-248.47 1357.16+/-1303.29 N1=40, N2=168 Fold Change: 2.31 P-value: 0	X	461.09+/-251.24 2636.53+/-3163.86 N1=40, N2=6 Fold Change: 3.81 P-value: .03322	461.09+/-251.24 1444.29+/-1485.46 N1=40, N2=31 Fold Change: 2.32 P-value: .00007	X
427	798	AI939507	X	X	X	X	67.26+/-38.98 211.34+/-144.81 N1=40, N2=10 Fold Change: 2.91 P-value: .00102

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
428	803	AI950023	X	X	X	335.59+/-291.5 129.73+/-80.19 N1=40, N2=31 Fold Change: 2.04 P-value: .00084	335.59+/-291.5 94.45+/-69.77 N1=40, N2=10 Fold Change: 2.9 P-value: .00112
429	805	AI952965	X	X	X	161.89+/-108.6 347.01+/-159.99 N1=40, N2=31 Fold Change: 2.38 P-value: 0	161.89+/-108.6 461.65+/-262.27 N1=40, N2=10 Fold Change: 2.78 P-value: .00455
430	806	AI953053	X	X	X	X	96.66+/-61.58 403.41+/-323.73 N1=40, N2=10 Fold Change: 3.33 P-value: .00265
431	808	AI954874	X	X	209.46+/-107.86 96.19+/-23.42 N1=40, N2=6 Fold Change: 2.01 P-value: .00017	X	X
432	810	AI961206	X	X	X	46.06+/-77.63 204.28+/-102.33 N1=40, N2=31 Fold Change: 3.96 P-value: 0	46.06+/-77.63 225.27+/-103.4 N1=40, N2=10 Fold Change: 4.13 P-value: .00043
433	817	AI968379	296.71+/-383.1 45.24+/-243.3 N1=40, N2=168 Fold Change: 4.99 P-value: 0	X	X	295.46+/-388.02 104.96+/-424.91 N1=40, N2=31 Fold Change: 4.47 P-value: .00001	295.46+/-388.02 -12.25+/-22.65 N1=40, N2=10 Fold Change: 6.3 P-value: 0
434	818	AI968904	744.48+/-291.11 370.58+/-143.78 N1=40, N2=168 Fold Change: 2 P-value: 0	X	X	738.79+/-292.65 373.44+/-151.46 N1=40, N2=31 Fold Change: 2.01 P-value: 0	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
435	822	AI970898	505.69+/-422.11 142.34+/-84.59 N1=40, N2=168 Fold Change: 3.33 P-value: 0	X	509.53+/-426.92 155.46+/-70.61 N1=40, N2=6 Fold Change: 2.81 P-value: .00097	509.53+/-426.92 116.99+/-60.55 N1=40, N2=31 Fold Change: 3.87 P-value: 0	509.53+/-426.92 117.04+/-63.48 N1=40, N2=10 Fold Change: 3.88 P-value: 0
436	823	AI971441	X	X	224.36+/-258.15 25.49+/-91 N1=40, N2=6 Fold Change: 3.79 P-value: .01447	224.36+/-258.15 44.4+/-132.79 N1=40, N2=31 Fold Change: 2.75 P-value: .0003	224.36+/-258.15 -63.46+/-142.66 N1=40, N2=10 Fold Change: 4.45 P-value: .0004
437	827	AI971914	X	X	X	X	121.63+/-64.27 329.2+/-298.85 N1=40, N2=10 Fold Change: 2.25 P-value: .00832
438	830	AI972498	285.82+/-111.27 134.28+/-71.62 N1=40, N2=168 Fold Change: 2.22 P-value: 0	X	X	286.51+/-112.64 124.7+/-61.16 N1=40, N2=31 Fold Change: 2.3 P-value: 0	286.51+/-112.64 109.37+/-47.71 N1=40, N2=10 Fold Change: 2.7 P-value: .00057
439	831	AI972661	X	X	X	482.12+/-600.67 177.9+/-209.56 N1=40, N2=31 Fold Change: 2.24 P-value: .01047	X
440	832	AI972873	437.97+/-212.54 117.56+/-101.2 N1=40, N2=168 Fold Change: 4.55 P-value: 0	X	436.16+/-215 164.58+/-155.74 N1=40, N2=6 Fold Change: 3.37 P-value: .021	436.16+/-215 126.68+/-109.81 N1=40, N2=31 Fold Change: 4.14 P-value: 0	436.16+/-215 75.01+/-128.01 N1=40, N2=10 Fold Change: 8.78 P-value: .00006
441	836	AI979261	X	X	X	145.88+/-125.11 301.16+/-194.23 N1=40, N2=31 Fold Change: 2.17 P-value: .00002	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
442	837	AI982669	X	X	X	352.73+/-154.77 769.65+/-400.6 N1=39, N2=31 Fold Change: 2.11 P-value: 0	352.73+/-154.77 839.63+/-451.94 N1=39, N2=6 Fold Change: 2.2 P-value: .00452
443	838	AI983045	282.14+/-333.79 -2.89+/-61.5 N1=40, N2=168 Fold Change: 6.23 P-value: 0	X	281.02+/-338.08 6.46+/-26.18 N1=40, N2=6 Fold Change: 6.38 P-value: 0	281.02+/-338.08 -12.28+/-33.2 N1=40, N2=31 Fold Change: 6.91 P-value: 0	281.02+/-338.08 -25.74+/-23.32 N1=40, N2=10 Fold Change: 7.49 P-value: 0
444	840	AI985653	X	X	X	243.4+/-112.77 111.29+/-55.01 N1=39, N2=31 Fold Change: 2.12 P-value: 0	243.4+/-112.77 81.33+/-38.99 N1=39, N2=6 Fold Change: 2.93 P-value: 0
445	841	AI989588	X	X	160.57+/-119.71 240.25+/-78.81 N1=40, N2=6 Fold Change: 2.01 P-value: .00445	X	X
446	846	AI990483	X	X	X	35.21+/-34.58 207.82+/-290.06 N1=40, N2=31 Fold Change: 2.5 P-value: .00091	X
447	853	AL031846	446.58+/-157.69 203.55+/-90.87 N1=40, N2=168 Fold Change: 2.21 P-value: 0	X	X	446.58+/-157.69 182.45+/-74.24 N1=40, N2=31 Fold Change: 2.41 P-value: 0	446.58+/-157.69 148.67+/-68.99 N1=40, N2=10 Fold Change: 3.01 P-value: .00002
448	855	AL037368	X	X	X	X	576.75+/-132.07 296.15+/-132.55 N1=40, N2=10 Fold Change: 2.12 P-value: .0014

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
449	857	AL037805	624.14+/-319.31 281.94+/-168.3 N1=40, N2=168 Fold Change: 2.29 P-value: 0	X	X	614.2+/-317.15 258.58+/-142.99 N1=40, N2=31 Fold Change: 2.38 P-value: 0	614.2+/-317.15 168.59+/-62.09 N1=40, N2=10 Fold Change: 3.3 P-value: 0
450	860	AL039445	X	X	X	X	103.65+/-39.97 204.36+/-54.58 N1=40, N2=10 Fold Change: 2.03 P-value: 0
451	861	AL039870	229.33+/-119.68 104.08+/-62.24 N1=40, N2=168 Fold Change: 2.19 P-value: 0	X	X	226.4+/-119.79 95.07+/-69.54 N1=40, N2=31 Fold Change: 2.41 P-value: 0	226.4+/-119.79 85.61+/-45.98 N1=40, N2=10 Fold Change: 2.58 P-value: .0005
452	862	AL039917	X	X	X	X	190.41+/-139.22 427.64+/-204.38 N1=40, N2=10 Fold Change: 2.48 P-value: .00467
453	864	AL040178	277.18+/-128.12 73.94+/-56.64 N1=39, N2=168 Fold Change: 3.48 P-value: 0	X	277.18+/-128.12 106.38+/-90.67 N1=39, N2=10 Fold Change: 2.79 P-value: .01209	277.18+/-128.12 59.11+/-47.84 N1=39, N2=31 Fold Change: 3.76 P-value: 0	277.18+/-128.12 44.44+/-29.67 N1=39, N2=6 Fold Change: 4.57 P-value: 0
454	865	AL040912	311.14+/-137.52 86.94+/-86.46 N1=40, N2=168 Fold Change: 4.08 P-value: 0	X	X	304.56+/-132.78 69.8+/-53.68 N1=40, N2=31 Fold Change: 4.66 P-value: 0	304.56+/-132.78 52.07+/-61.09 N1=40, N2=10 Fold Change: 6.69 P-value: .00001
455	866	AL041815	257.28+/-104.74 129.57+/-68.69 N1=40, N2=168 Fold Change: 2.04 P-value: 0	X	X	257.35+/-106.11 124.69+/-56.27 N1=40, N2=31 Fold Change: 2 P-value: 0	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
456	**867**	**AL042492**	801.96+/-843.5 56.95+/-101.91 N1=40, N2=168 Fold Change: 12.71 P-value: 0	X	809.69+/-853.09 101.65+/-170.57 N1=40, N2=6 Fold Change: 8.78 P-value: .00362	809.69+/-853.09 40.59+/-106.87 N1=40, N2=31 Fold Change: 15 P-value: 0	809.69+/-853.09 11.79+/-18.8 N1=40, N2=10 Fold Change: 20.99 P-value: 0
457	**868**	**AL042923**	X	X	X	X	3125.4+/-1239.9 1575.01+/-724.4 N1=40, N2=10 Fold Change: 2.07 P-value: .00207
458	**870**	**AL043980**	X	X	X	498.96+/-198.25 248.27+/-101.89 N1=40, N2=31 Fold Change: 2.06 P-value: 0	498.96+/-198.25 206.45+/-96.76 N1=40, N2=10 Fold Change: 2.43 P-value: .00002
459	**871**	**AL044366**	137.98+/-186.9 313.36+/-363.79 N1=40, N2=168 Fold Change: 2.23 P-value: .00018	X	X	X	X
460	**872**	**AL044613**	X	X	X	X	304+/-112.89 102.49+/-79.71 N1=40, N2=10 Fold Change: 3.15 P-value: .00076
461	**876**	**AL046941**	425.75+/-236.48 53.79+/-102.7 N1=40, N2=168 Fold Change: 8.01 P-value: 0	X	X	428.58+/-238.89 34.11+/-80.54 N1=40, N2=31 Fold Change: 9.66 P-value: 0	428.58+/-238.89 -23.64+/-33.24 N1=40, N2=10 Fold Change: 16.81 P-value: 0
462	**877**	**AL046946**	X	X	X	X	713.56+/-217.52 287.87+/-116 N1=40, N2=10 Fold Change: 2.57 P-value: .00006

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
463	878	AL048304	X	X	X	X	308.79+/-74.62 97.9+/-114.69 N1=40, N2=10 Fold Change: 3.99 P-value: .00402
464	879	AL048386	233.2+/-107.71 118.45+/-83.53 N1=40, N2=168 Fold Change: 2.19 P-value: 0	X	X	232.52+/-109.03 94.13+/-59.17 N1=40, N2=31 Fold Change: 2.63 P-value: 0	232.52+/-109.03 73.94+/-51.55 N1=40, N2=10 Fold Change: 3.32 P-value: .00019
465	880	AL048399	X	X	X	768.94+/-280.35 336.8+/-159.66 N1=40, N2=31 Fold Change: 2.37 P-value: 0	768.94+/-280.35 378.81+/-201.68 N1=40, N2=10 Fold Change: 2.22 P-value: .00292
466	881	AL048962	951.97+/-353.33 498.61+/-346.17 N1=40, N2=168 Fold Change: 2.03 P-value: 0	X	X	944+/-354.29 469.14+/-334.1 N1=40, N2=31 Fold Change: 2.17 P-value: 0	944+/-354.29 400.6+/-283.17 N1=40, N2=10 Fold Change: 2.45 P-value: .00012
467	883	AL049257	X	X	X	258.77+/-104.32 110.97+/-53.29 N1=40, N2=31 Fold Change: 2.35 P-value: 0	258.77+/-104.32 104.27+/-37.82 N1=40, N2=10 Fold Change: 2.34 P-value: 0
468	884	AL049423	X	X	X	385.45+/-146.45 176.43+/-82.21 N1=40, N2=31 Fold Change: 2.19 P-value: 0	385.45+/-146.45 131.88+/-33.79 N1=40, N2=10 Fold Change: 2.73 P-value: 0
469	885	AL049471	X	X	X	585.55+/-164.83 312.66+/-134.95 N1=40, N2=31 Fold Change: 2.01 P-value: 0	585.55+/-164.83 304.04+/-127.09 N1=40, N2=10 Fold Change: 2.01 P-value: .00064

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
470	887	AL049949	X	X	X	525.51+/-234.08 218.01+/-118.84 N1=40, N2=31 Fold Change: 2.27 P-value: 0	525.51+/-234.08 184.51+/-151.36 N1=40, N2=10 Fold Change: 3.21 P-value: .00178
471	888	AL049957	X	X	X	664.06+/-250.51 339.26+/-164.3 N1=39, N2=31 Fold Change: 1.98 P-value: 0	X
472	890	AL050002	X	X	X	X	320.95+/-114.96 152.33+/-60.11 N1=40, N2=10 Fold Change: 2.08 P-value: .00017
473	893	AL050367	257.59+/-77.75 155+/-120.63 N1=40, N2=168 Fold Change: 2 P-value: 0	X	X	257.59+/-77.75 117.16+/-76.86 N1=40, N2=31 Fold Change: 2.49 P-value: 0	X
474	894	AL079279	313.49+/-189.76 108.29+/-83.88 N1=40, N2=168 Fold Change: 2.87 P-value: 0	X	313.49+/-189.76 114+/-76.08 N1=40, N2=6 Fold Change: 2.51 P-value: .00823	313.49+/-189.76 86.73+/-51.4 N1=40, N2=31 Fold Change: 3.29 P-value: 0	313.49+/-189.76 49.04+/-28.4 N1=40, N2=10 Fold Change: 5.69 P-value: 0
475	896	AL079707	258.01+/-224.37 67.86+/-48.3 N1=40, N2=168 Fold Change: 3.55 P-value: 0	X	261.69+/-226.08 82.89+/-41.99 N1=40, N2=6 Fold Change: 2.73 P-value: .0013	261.69+/-226.08 48.17+/-30.27 N1=40, N2=31 Fold Change: 4.63 P-value: 0	261.69+/-226.08 78.83+/-21.26 N1=40, N2=10 Fold Change: 2.7 P-value: 0
476	897	AL079769	198.26+/-265.48 337.38+/-218.01 N1=40, N2=168 Fold Change: 2.06 P-value: 0	X	X	201.74+/-268.02 451.36+/-269.91 N1=40, N2=31 Fold Change: 2.73 P-value: 0	201.74+/-268.02 415.85+/-142.87 N1=40, N2=10 Fold Change: 2.88 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
477	898	AL079949	X	X	X	382.36+/-135.98 172.14+/-65.04 N1=40, N2=31 Fold Change: 2.21 P-value: 0	382.36+/-135.98 160.74+/-65.7 N1=40, N2=10 Fold Change: 2.34 P-value: .00001
478	899	AL080192	X	X	X	103.54+/-69.27 242.17+/-111.66 N1=40, N2=31 Fold Change: 2.54 P-value: 0	X
479	903	AL120446	304.54+/-95.79 151.01+/-51.13 N1=40, N2=168 Fold Change: 2 P-value: 0	X	X	302.81+/-96.4 143.68+/-46.25 N1=40, N2=31 Fold Change: 2.07 P-value: 0	302.81+/-96.4 137.13+/-46.57 N1=40, N2=10 Fold Change: 2.16 P-value: .00001
480	904	AW000899	255.52+/-122.34 125.26+/-107.3 N1=39, N2=168 Fold Change: 2.23 P-value: 0	X	X	255.52+/-122.34 136.12+/-122.63 N1=39, N2=31 Fold Change: 2.06 P-value: .00003	X
481	907	AW002846	282.39+/-199.06 139.23+/-115.04 N1=40, N2=168 Fold Change: 2.15 P-value: 0	X	X	X	283.14+/-201.6 97.8+/-63.96 N1=40, N2=10 Fold Change: 2.7 P-value: .00045
482	912	AW003362	X	X	211.57+/-81.24 89.06+/-83.95 N1=39, N2=10 Fold Change: 2.32 P-value: .02046	X	X
483	914	AW005418	X	X	X	205.57+/-234.3 67.1+/-110.71 N1=40, N2=31 Fold Change: 2.41 P-value: .00083	205.57+/-234.3 10.33+/-83.48 N1=40, N2=10 Fold Change: 3.7 P-value: .00052

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
484	915	AW005814	X	X	146.08+/-90.43 310.43+/-106.68 N1=40, N2=6 Fold Change: 2.4 P-value: .00072	X	X
485	916	AW006235	344.79+/-207.97 103.81+/-60.65 N1=40, N2=168 Fold Change: 3.17 P-value: 0	X	346.9+/-210.26 126.57+/-35.39 N1=40, N2=6 Fold Change: 2.35 P-value: .00014	346.9+/-210.26 95.72+/-56.93 N1=40, N2=31 Fold Change: 3.43 P-value: 0	346.9+/-210.26 99.92+/-23.08 N1=40, N2=10 Fold Change: 2.94 P-value: 0
486	919	AW006898	841.88+/-394.55 331.12+/-203.65 N1=40, N2=168 Fold Change: 2.68 P-value: 0	X	X	835.42+/-397.56 305.25+/-163.97 N1=40, N2=31 Fold Change: 2.7 P-value: 0	835.42+/-397.56 305.65+/-212.32 N1=40, N2=10 Fold Change: 2.91 P-value: .00883
487	920	AW006998	X	X	X	79.75+/-104.09 221.43+/-283.12 N1=40, N2=31 Fold Change: 2.76 P-value: .00002	X
488	921	AW007080	226.13+/-116.85 62.58+/-55.91 N1=40, N2=168 Fold Change: 3.65 P-value: 0	X	X	223.2+/-116.87 55.48+/-39.27 N1=40, N2=31 Fold Change: 3.79 P-value: 0	223.2+/-116.87 48.27+/-49.28 N1=40, N2=10 Fold Change: 4.6 P-value: .00008
489	925	AW007586	552.57+/-493.88 992.94+/-672.01 N1=40, N2=168 Fold Change: 2.04 P-value: .00003	X	X	552.57+/-493.88 1388.39+/-797.65 N1=40, N2=31 Fold Change: 2.99 P-value: 0	X
490	927	AW007983	308.57+/-180.09 124.89+/-104.9 N1=39, N2=168 Fold Change: 2.45 P-value: 0	X	308.57+/-180.09 120.02+/-133.67 N1=39, N2=10 Fold Change: 3.11 P-value: .02642	308.57+/-180.09 98.43+/-60.3 N1=39, N2=31 Fold Change: 2.82 P-value: 0	308.57+/-180.09 57.05+/-49.19 N1=39, N2=6 Fold Change: 4.11 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
491	929	AW009505	X	X	X	X	210.48+/-63.01 452.13+/-225.92 N1=40, N2=10 Fold Change: 2.06 P-value: .00023
492	930	AW013949	X	X	228.98+/-140.11 526.51+/-241.81 N1=40, N2=6 Fold Change: 2.49 P-value: .00743	X	X
493	932	AW014647	222.93+/-95.23 93.53+/-66.06 N1=39, N2=168 Fold Change: 2.35 P-value: 0	X	X	222.93+/-95.23 87.53+/-67.66 N1=39, N2=31 Fold Change: 2.48 P-value: 0	222.93+/-95.23 103.61+/-77.88 N1=39, N2=6 Fold Change: 2.1 P-value: .00171
494	933	AW014764	299.88+/-160.3 148.29+/-123.67 N1=39, N2=168 Fold Change: 2.02 P-value: 0	X	X	299.88+/-160.3 143.2+/-104.38 N1=39, N2=31 Fold Change: 2.02 P-value: 0	X
495	934	AW015571	X	X	X	X	648.86+/-400.58 174.43+/-228.74 N1=40, N2=10 Fold Change: 6.15 P-value: .00262
496	938	AW021108	220.45+/-143.17 97.68+/-75.55 N1=39, N2=168 Fold Change: 2.37 P-value: 0	X	X	220.45+/-143.17 87.82+/-65.1 N1=39, N2=31 Fold Change: 2.67 P-value: 0	220.45+/-143.17 76.42+/-41.74 N1=39, N2=6 Fold Change: 2.68 P-value: .00045
497	939	AW021169	256.18+/-141.26 128.88+/-175.65 N1=40, N2=168 Fold Change: 2.2 P-value: 0	X	X	X	254.1+/-142.48 131+/-172.12 N1=40, N2=10 Fold Change: 2.58 P-value: .00997

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
498	941	AW022607	X	X	X	820.58+/-231.5 436.42+/-247.61 N1=40, N2=31 Fold Change: 2.16 P-value: 0	820.58+/-231.5 384.68+/-242.39 N1=40, N2=10 Fold Change: 2.39 P-value: .00116
499	943	AW023188	X	X	X	290.36+/-132.68 130.36+/-49.53 N1=39, N2=31 Fold Change: 2.07 P-value: 0	X
500	945	AW024285	X	X	X	X	250.28+/-98.87 572.73+/-295.31 N1=40, N2=10 Fold Change: 2.27 P-value: .00009
501	946	AW024434	790.91+/-331.85 432.05+/-300.27 N1=40, N2=168 Fold Change: 2.03 P-value: 0	X	X	789.9+/-336.13 365.21+/-203.57 N1=40, N2=31 Fold Change: 2.21 P-value: 0	X
502	948	AW024795	X	X	X	X	194.61+/-162.76 374.26+/-130.52 N1=40, N2=10 Fold Change: 2.22 P-value: .00004
503	952	AW044663	X	X	X	X	216.92+/-78.22 104.46+/-39.86 N1=40, N2=10 Fold Change: 2.01 P-value: .00001
504	953	AW051492	440.5+/-328.97 200.34+/-109.37 N1=40, N2=168 Fold Change: 2.03 P-value: 0	X	X	442.65+/-332.99 174.66+/-95.13 N1=40, N2=31 Fold Change: 2.4 P-value: 0	442.65+/-332.99 133.38+/-80.06 N1=40, N2=10 Fold Change: 3.04 P-value: .00008

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
505	**955**	**AW052186**	200.32+/-119.43 68.25+/-52.36 N1=39, N2=168 Fold Change: 2.47 P-value: 0	X	200.32+/-119.43 83.05+/-58.17 N1=39, N2=10 Fold Change: 2.54 P-value: .0089	200.32+/-119.43 62.34+/-42.9 N1=39, N2=31 Fold Change: 2.68 P-value: 0	200.32+/-119.43 45.67+/-44.89 N1=39, N2=6 Fold Change: 3.64 P-value: .00001
506	**956**	**C16443**	470.61+/-305.63 179.69+/-105 N1=40, N2=168 Fold Change: 2.63 P-value: 0	X	470.75+/-309.62 197.91+/-113.36 N1=40, N2=6 Fold Change: 2.24 P-value: .00778	470.75+/-309.62 144.75+/-66.63 N1=40, N2=31 Fold Change: 3.13 P-value: 0	470.75+/-309.62 143.41+/-109.79 N1=40, N2=10 Fold Change: 3.49 P-value: .00031
507	**957**	**C17781**	233.51+/-142.32 116.34+/-81.47 N1=40, N2=168 Fold Change: 2.05 P-value: 0	X	X	X	X
508	**967**	**D55884**	X	X	X	231.13+/-145.06 105.18+/-64.42 N1=40, N2=31 Fold Change: 2.13 P-value: .00004	X
509	**970**	**D63177**	72.4+/-72.56 225.06+/-178.61 N1=40, N2=168 Fold Change: 3.08 P-value: 0	X	X	X	X
510	**971**	**D79487**	X	X	X	X	215.9+/-67.18 84.24+/-31.19 N1=39, N2=6 Fold Change: 2.6 P-value: .00001
511	**981**	**H11724**	X	X	X	321.52+/-187.56 158.38+/-76 N1=40, N2=31 Fold Change: 2 P-value: 0	321.52+/-187.56 124.97+/-54.73 N1=40, N2=10 Fold Change: 2.5 P-value: .00011

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
512	983	H15868	347.4+/-390.17 933.09+/-1186.46 N1=40, N2=168 Fold Change: 2.13 P-value: .00049	X	344.41+/-394.81 967.69+/-1057.17 N1=40, N2=6 Fold Change: 3.28 P-value: .02477	X	X
513	984	H16294	X	X	X	X	812.95+/-387.97 295.8+/-82.15 N1=40, N2=10 Fold Change: 2.51 P-value: 0
514	985	H16568	293.47+/-211.85 64.62+/-58.27 N1=40, N2=168 Fold Change: 3.74 P-value: 0	X	X	288.53+/-212.27 46.38+/-45.45 N1=40, N2=31 Fold Change: 4.69 P-value: 0	288.53+/-212.27 38.38+/-26.86 N1=40, N2=10 Fold Change: 5.41 P-value: 0
515	987	H27948	221.34+/-117.87 86.49+/-44.22 N1=39, N2=168 Fold Change: 2.46 P-value: 0	X	X	221.34+/-117.87 80.01+/-37.66 N1=39, N2=31 Fold Change: 2.42 P-value: 0	221.34+/-117.87 76.82+/-36.99 N1=39, N2=6 Fold Change: 2.75 P-value: .00004
516	990	H42085	X	X	X	X	405.54+/-244.99 174.03+/-102.69 N1=40, N2=10 Fold Change: 2.17 P-value: .00064
517	991	H43374	X	X	X	X	588.83+/-221.87 314.31+/-230.39 N1=40, N2=10 Fold Change: 2.1 P-value: .00493
518	992	H54254	370.85+/-679.27 33.63+/-58.23 N1=40, N2=168 Fold Change: 5.23 P-value: 0	X	377.04+/-687.01 31.69+/-34.95 N1=40, N2=6 Fold Change: 4.88 P-value: .00045	377.04+/-687.01 21.83+/-62.85 N1=40, N2=31 Fold Change: 6.53 P-value: 0	377.04+/-687.01 12.93+/-28.05 N1=40, N2=10 Fold Change: 6.25 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
519	993	H58608	202.11+/-137.98 82.39+/-48.64 N1=40, N2=168 Fold Change: 2.25 P-value: 0	X	X	201.08+/-139.62 64.47+/-33.26 N1=40, N2=31 Fold Change: 2.77 P-value: 0	201.08+/-139.62 53.32+/-25 N1=40, N2=10 Fold Change: 3.21 P-value: 0
520	1061	N21030	X	X	X	822.97+/-445.6 356.31+/-294.65 N1=40, N2=31 Fold Change: 2.5 P-value: .00002	X
521	1064	N21424	X	X	X	X	344.38+/-141.72 134.11+/-57.31 N1=40, N2=10 Fold Change: 2.56 P-value: .00005
522	1066	N24987	X	X	X	92.04+/-95.24 206.91+/-82.99 N1=40, N2=31 Fold Change: 2.71 P-value: 0	92.04+/-95.24 210.74+/-113.1 N1=40, N2=10 Fold Change: 2.65 P-value: .00009
523	1067	N25096	X	X	X	X	308.47+/-138.2 118.5+/-63.44 N1=40, N2=10 Fold Change: 2.77 P-value: .00098
524	1068	N25267	26.22+/-51.01 217.96+/-178.06 N1=40, N2=168 Fold Change: 5.07 P-value: 0	X	X	X	X
525	1071	N31946	X	X	X	X	156.39+/-61.76 332.92+/-151.29 N1=40, N2=10 Fold Change: 2.11 P-value: .00022

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
526	1072	N32254	X	X	X	X	116.51+/-51.56 249.15+/-168.21 N1=40, N2=10 Fold Change: 2.03 P-value: .0051
527	1074	N42752	63.26+/-47.52 203.51+/-259.92 N1=40, N2=168 Fold Change: 2.23 P-value: 0	X	X	63.77+/-48.02 251.31+/-284.54 N1=40, N2=31 Fold Change: 2.74 P-value: .00008	X
528	1075	N45224	X	X	X	X	574.83+/-196.53 208.47+/-108.26 N1=40, N2=10 Fold Change: 2.79 P-value: .00004
529	1076	N45320	365.77+/-123.03 164.05+/-84.04 N1=40, N2=168 Fold Change: 2.35 P-value: 0	X	X	359.46+/-117.88 163.46+/-78.87 N1=40, N2=31 Fold Change: 2.36 P-value: 0	359.46+/-117.88 150.13+/-52.84 N1=40, N2=10 Fold Change: 2.34 P-value: .00001
530	1079	N48809	X	X	130.33+/-82.96 233.51+/-111.27 N1=40, N2=6 Fold Change: 2.03 P-value: .00829	X	130.33+/-82.96 249.11+/-95.4 N1=40, N2=10 Fold Change: 2.14 P-value: .00153
531	1082	N51335	X	X	X	108.78+/-93.56 222.06+/-201.45 N1=40, N2=31 Fold Change: 2 P-value: .00003	X
532	1083	N52086	289.83+/-310.5 106.77+/-102.27 N1=40, N2=168 Fold Change: 2.07 P-value: .00114	X	X	289.83+/-310.5 95.72+/-73.59 N1=40, N2=31 Fold Change: 2.16 P-value: .00247	289.83+/-310.5 77.86+/-63.6 N1=40, N2=10 Fold Change: 2.55 P-value: .0038

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
533	1084	N52352	X	X	X	X	268.01+/-82.24 136.43+/-64.33 N1=40, N2=10 Fold Change: 2.09 P-value: .0074
534	1085	N56877	109.5+/-80.79 309.93+/-270.27 N1=40, N2=168 Fold Change: 2.45 P-value: 0	X	X	109.5+/-80.79 327.79+/-348.66 N1=40, N2=31 Fold Change: 2.15 P-value: .00281	109.5+/-80.79 306.18+/-259.39 N1=40, N2=10 Fold Change: 2.68 P-value: .00382
535	1086	N57539	225.43+/-101.42 103.31+/-100.1 N1=39, N2=168 Fold Change: 2.37 P-value: 0	X	X	225.43+/-101.42 106.35+/-190.86 N1=39, N2=31 Fold Change: 2.94 P-value: 0	225.43+/-101.42 96.95+/-76.68 N1=39, N2=6 Fold Change: 2.43 P-value: .00273
536	1087	N59432	X	X	237.95+/-107.53 71.26+/-38.6 N1=39, N2=10 Fold Change: 3.32 P-value: .00159	237.95+/-107.53 105.02+/-65.3 N1=39, N2=31 Fold Change: 2.39 P-value: 0	237.95+/-107.53 110.93+/-111.49 N1=39, N2=6 Fold Change: 2.61 P-value: .00543
537	1088	N62126	X	X	X	X	280.04+/-181.07 109.11+/-74.94 N1=40, N2=10 Fold Change: 2.59 P-value: .00734
538	1089	N63237	217.51+/-156.97 63.12+/-54.35 N1=39, N2=168 Fold Change: 2.55 P-value: 0	X	217.51+/-156.97 52.65+/-34.21 N1=39, N2=10 Fold Change: 3.16 P-value: .00096	217.51+/-156.97 52.57+/-33.35 N1=39, N2=31 Fold Change: 2.9 P-value: 0	217.51+/-156.97 24.34+/-38.62 N1=39, N2=6 Fold Change: 3.83 P-value: .00001
539	1090	N63913	463.66+/-314.65 88.17+/-134.91 N1=40, N2=168 Fold Change: 5.84 P-value: 0	X	X	458.01+/-316.71 87.05+/-105.81 N1=40, N2=31 Fold Change: 5.25 P-value: 0	458.01+/-316.71 65.18+/-127.89 N1=40, N2=10 Fold Change: 7.57 P-value: .00008

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
540	1091	N64648	X	X	X	262.87+/-87.71 129.76+/-54.11 N1=40, N2=31 Fold Change: 2.09 P-value: 0	262.87+/-87.71 114.48+/-29.26 N1=40, N2=10 Fold Change: 2.21 P-value: 0
541	1092	N76867	X	X	X	210.78+/-96.34 106.18+/-57.67 N1=39, N2=31 Fold Change: 1.97 P-value: 0	X
542	1094	N79004	X	X	X	X	93.29+/-75.16 273.05+/-182.9 N1=40, N2=10 Fold Change: 2.79 P-value: .00222
543	1095	N80935	266.86+/-83.21 143.94+/-87.39 N1=40, N2=168 Fold Change: 2.01 P-value: 0	X	X	X	266.66+/-84.29 130.9+/-68.88 N1=40, N2=10 Fold Change: 2.17 P-value: .00097
544	1096	N90525	117.6+/-226.89 226.51+/-203.72 N1=40, N2=168 Fold Change: 2.23 P-value: .00001	X	X	118.22+/-229.82 255.32+/-119.15 N1=40, N2=31 Fold Change: 2.98 P-value: 0	X
545	1101	R08000	501.45+/-685.59 78.58+/-101 N1=40, N2=168 Fold Change: 4.96 P-value: 0	X	502.76+/-694.51 79.82+/-77.61 N1=40, N2=6 Fold Change: 4.45 P-value: .0049	502.76+/-694.51 57.68+/-127.95 N1=40, N2=31 Fold Change: 7.21 P-value: 0	502.76+/-694.51 65.51+/-107.84 N1=40, N2=10 Fold Change: 6.92 P-value: .00004
546	1102	R11248	X	X	X	114.31+/-112.68 295.22+/-374.37 N1=40, N2=31 Fold Change: 2.09 P-value: .00187	114.31+/-112.68 538.23+/-597.4 N1=40, N2=10 Fold Change: 3.42 P-value: .01362

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
547	**1104**	**R20784**	1107.23+/-833.81 264.46+/-256.11 N1=40, N2=168 Fold Change: 4.88 P-value: 0	X	1112.78+/-843.96 257.86+/-243.05 N1=40, N2=6 Fold Change: 4.54 P-value: .00794	1112.78+/-843.96 168.78+/-236.94 N1=40, N2=31 Fold Change: 7.78 P-value: 0	1112.78+/-843.96 123.27+/-153.07 N1=40, N2=10 Fold Change: 10.71 P-value: .00001
548	**1109**	**R49392**	X	X	X	267.35+/-98.92 156.98+/-110.51 N1=40, N2=31 Fold Change: 2.05 P-value: .00002	267.35+/-98.92 143.02+/-95.35 N1=40, N2=10 Fold Change: 2.14 P-value: .0067
549	**1112**	**R54660**	X	X	200.26+/-133.86 49.74+/-62.98 N1=40, N2=6 Fold Change: 4.34 P-value: .00827	200.26+/-133.86 16.03+/-23.1 N1=40, N2=31 Fold Change: 5.96 P-value: 0	200.26+/-133.86 6.98+/-15.78 N1=40, N2=10 Fold Change: 6.74 P-value: 0
550	**1113**	**R62346**	92.55+/-48.64 218.35+/-108.48 N1=39, N2=168 Fold Change: 2.17 P-value: 0	X	X	92.55+/-48.64 218.34+/-122.05 N1=39, N2=31 Fold Change: 2.14 P-value: 0	X
551	**1114**	**R67627**	X	X	X	703.42+/-425.8 319.29+/-199.18 N1=40, N2=31 Fold Change: 2.32 P-value: 0	X
552	**1115**	**R69584**	211.19+/-227.25 53.06+/-91.11 N1=40, N2=168 Fold Change: 2.91 P-value: .00001	X	214.32+/-229.35 30.89+/-23.04 N1=40, N2=6 Fold Change: 3.38 P-value: .0002	214.32+/-229.35 37.79+/-84.48 N1=40, N2=31 Fold Change: 3.62 P-value: 0	214.32+/-229.35 6.84+/-26.67 N1=40, N2=10 Fold Change: 4.76 P-value: 0
553	**1116**	**R70255**	241.03+/-179.01 33.3+/-86.44 N1=40, N2=168 Fold Change: 5.3 P-value: 0	X	X	241.29+/-181.34 25.72+/-39.39 N1=40, N2=31 Fold Change: 5.24 P-value: 0	241.29+/-181.34 17.97+/-75.13 N1=40, N2=10 Fold Change: 5.55 P-value: .00003

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
554	1117	R73518	397.68+/-234.48 142.17+/-86.32 N1=39, N2=168 Fold Change: 2.61 P-value: 0	X	X	397.68+/-234.48 129.97+/-75.3 N1=39, N2=31 Fold Change: 2.92 P-value: 0	397.68+/-234.48 130.92+/-91.05 N1=39, N2=6 Fold Change: 2.93 P-value: .00003
555	1118	R74561	X	X	X	425.23+/-350.96 871.35+/-705.04 N1=40, N2=31 Fold Change: 2.06 P-value: .00036	X
556	1119	R83604	294.9+/-858.81 -49.34+/-85.75 N1=40, N2=168 Fold Change: 3.18 P-value: .00005	X	304.76+/-867.74 -70.76+/-37.34 N1=40, N2=6 Fold Change: 3.74 P-value: .00001	304.76+/-867.74 -62.65+/-38.9 N1=40, N2=31 Fold Change: 3.74 P-value: .00001	304.76+/-867.74 -42.74+/-57.17 N1=40, N2=10 Fold Change: 3.25 P-value: .0002
557	1121	T16144	X	X	X	67.72+/-60.08 246.32+/-239.25 N1=40, N2=31 Fold Change: 3.16 P-value: 0	67.72+/-60.08 213.1+/-108.52 N1=40, N2=10 Fold Change: 3.43 P-value: .00004
558	1122	T57042	X	X	X	286.11+/-193.74 114.39+/-69.74 N1=40, N2=31 Fold Change: 2.34 P-value: 0	286.11+/-193.74 125.4+/-63.01 N1=40, N2=10 Fold Change: 2.01 P-value: .00122
559	1123	T57670	X	X	X	404.19+/-128.46 212.97+/-107.98 N1=40, N2=31 Fold Change: 2.03 P-value: 0	404.19+/-128.46 186+/-108.03 N1=40, N2=10 Fold Change: 2.39 P-value: .00117
560	1124	T57773	X	X	X	X	214.22+/-119.35 76.17+/-87.27 N1=40, N2=10 Fold Change: 3.27 P-value: .002

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
561	**1125**	**T61106**	164.66+/-104.9 345.33+/-209.56 N1=39, N2=168 Fold Change: 2.21 P-value: .00001	X	X	164.66+/-104.9 339.88+/-198.04 N1=39, N2=31 Fold Change: 2.11 P-value: .00077	164.66+/-104.9 341.68+/-227.02 N1=39, N2=6 Fold Change: 2.17 P-value: .01513
562	**1126**	**T64447**	216.31+/-152.39 41.01+/-92.12 N1=39, N2=168 Fold Change: 3.99 P-value: 0	X	216.31+/-152.39 39.2+/-138.62 N1=39, N2=10 Fold Change: 3.8 P-value: .01694	216.31+/-152.39 17.71+/-47.39 N1=39, N2=31 Fold Change: 5.18 P-value: 0	216.31+/-152.39 -19.08+/-58.11 N1=39, N2=6 Fold Change: 7.39 P-value: 0
563	**1130**	**T79945**	266.46+/-143.28 196.1+/-275.3 N1=40, N2=168 Fold Change: 2.04 P-value: 0	X	X	X	X
564	**1133**	**T92947**	370.07+/-299.38 173.72+/-164.88 N1=40, N2=168 Fold Change: 2.08 P-value: .00004	X	X	359.82+/-296.09 134.2+/-88.77 N1=40, N2=31 Fold Change: 2.39 P-value: .00007	359.82+/-296.09 113.03+/-41.6 N1=40, N2=10 Fold Change: 2.36 P-value: .00008
565	**1134**	**T93570**	X	X	X	344.83+/-197.39 156.26+/-76.45 N1=40, N2=31 Fold Change: 2.12 P-value: 0	344.83+/-197.39 137.27+/-55.02 N1=40, N2=10 Fold Change: 2.27 P-value: .0001
566	**1170**	**W02608**	83.49+/-56.33 238.33+/-117.55 N1=40, N2=168 Fold Change: 3.06 P-value: 0	X	X	82.66+/-56.82 216.35+/-112.51 N1=40, N2=31 Fold Change: 2.77 P-value: 0	82.66+/-56.82 206.9+/-95.19 N1=40, N2=10 Fold Change: 2.61 P-value: .00124
567	**1171**	**W02823**	220.34+/-88.04 83.44+/-86.86 N1=40, N2=168 Fold Change: 2.96 P-value: 0	X	X	217.4+/-87.18 71.46+/-47.57 N1=40, N2=31 Fold Change: 3.16 P-value: 0	217.4+/-87.18 107.28+/-72.66 N1=40, N2=10 Fold Change: 2.32 P-value: .00987

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
568	1173	W07043	301.61+/-162.72 67.74+/-52.69 N1=40, N2=168 Fold Change: 4.19 P-value: 0	X	299.21+/-164.12 108.65+/-140.45 N1=40, N2=6 Fold Change: 3.51 P-value: .03256	299.21+/-164.12 56.2+/-41.66 N1=40, N2=31 Fold Change: 4.81 P-value: 0	299.21+/-164.12 49.97+/-36.95 N1=40, N2=10 Fold Change: 5.11 P-value: 0
569	1174	W07304	1144.81+/-440.02 379.83+/-343.79 N1=40, N2=168 Fold Change: 3.79 P-value: 0	X	X	1139.71+/-444.58 244.74+/-245.86 N1=40, N2=31 Fold Change: 5.59 P-value: 0	1139.71+/-444.58 291.49+/-262.25 N1=40, N2=10 Fold Change: 5.29 P-value: .00046
570	1177	W22264	X	X	X	X	172.41+/-85.84 443.37+/-353.68 N1=40, N2=10 Fold Change: 2.22 P-value: .00917
571	1181	W28281	X	X	X	314.68+/-111.87 147.05+/-53.04 N1=39, N2=31 Fold Change: 2.14 P-value: 0	X
572	1182	W31919	X	X	X	67.04+/-84.41 322.95+/-770.03 N1=40, N2=31 Fold Change: 2.05 P-value: .00441	X
573	1183	W32480	707.63+/-942.95 144.29+/-433.7 N1=40, N2=168 Fold Change: 5.42 P-value: 0	X	X	720.17+/-951.89 169.52+/-503.24 N1=40, N2=31 Fold Change: 4.62 P-value: 0	720.17+/-951.89 39.22+/-65.55 N1=40, N2=10 Fold Change: 7.71 P-value: 0
574	1189	W55924	X	X	X	X	100.04+/-68.17 213+/-119.61 N1=40, N2=10 Fold Change: 2.14 P-value: .00375

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
575	1195	W72062	381.86+/-163.16 182.13+/-62.01 N1=40, N2=168 Fold Change: 2.03 P-value: 0	X	X	380.68+/-165.12 175.84+/-50.18 N1=40, N2=31 Fold Change: 2.04 P-value: 0	380.68+/-165.12 176.3+/-66.81 N1=40, N2=10 Fold Change: 2.07 P-value: .00001
576	1196	W72182	X	X	X	X	83.09+/-49 231.34+/-134.05 N1=40, N2=10 Fold Change: 2.71 P-value: .00094
577	1199	W72347	367.98+/-155.29 146.12+/-193.47 N1=40, N2=168 Fold Change: 3.46 P-value: 0	X	X	368.08+/-157.32 94.65+/-155.82 N1=40, N2=31 Fold Change: 5.14 P-value: 0	368.08+/-157.32 261.92+/-468.76 N1=40, N2=10 Fold Change: 3.22 P-value: .03608
578	1200	W72407	235.27+/-157.67 63.55+/-76.04 N1=40, N2=168 Fold Change: 3.77 P-value: 0	X	X	234.77+/-159.7 85.52+/-101.27 N1=40, N2=31 Fold Change: 3.02 P-value: .00001	X
579	1201	W72511	995.7+/-434.28 430.04+/-283.24 N1=40, N2=168 Fold Change: 2.53 P-value: 0	X	X	988.5+/-437.53 418.47+/-331.96 N1=40, N2=31 Fold Change: 2.63 P-value: 0	988.5+/-437.53 250.59+/-208.45 N1=40, N2=10 Fold Change: 4.54 P-value: .00008
580	1203	W73230	526.33+/-307.22 205.2+/-108.64 N1=40, N2=168 Fold Change: 2.58 P-value: 0	X	X	524.48+/-311.01 185.59+/-79.06 N1=40, N2=31 Fold Change: 2.72 P-value: 0	524.48+/-311.01 164.36+/-67.2 N1=40, N2=10 Fold Change: 3 P-value: 0
581	1204	W73386	242.96+/-399.57 16.99+/-76.53 N1=40, N2=168 Fold Change: 4.25 P-value: 0	469.37+/-905.14 95.29+/-88.61 N1=17, N2=49 Fold Change: 3.43 P-value: .00019	248.29+/-403.35 3.09+/-55.26 N1=40, N2=6 Fold Change: 4.79 P-value: .00079	248.29+/-403.35 -16.75+/-32.9 N1=40, N2=31 Fold Change: 5.86 P-value: 0	248.29+/-403.35 -2.29+/-42.09 N1=40, N2=10 Fold Change: 4.92 P-value: 0

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs Stage I	Normal vs Stage II	Normal vs Stage III
582	1205	W73819	X	X	X	993.58+/-625.18 399.14+/-205.47 N1=40, N2=31 Fold Change: 2.23 P-value: 0	993.58+/-625.18 277.46+/-140.58 N1=40, N2=10 Fold Change: 3.36 P-value: .00039
583	1206	W73855	X	X	X	201.45+/-105.43 87.02+/-86.49 N1=40, N2=31 Fold Change: 2.72 P-value: 0	X
584	1207	W73890	223.3+/-129.09 73.33+/-44.79 N1=40, N2=168 Fold Change: 2.96 P-value: 0	X	X	223.01+/-130.77 65.62+/-33.81 N1=40, N2=31 Fold Change: 3.14 P-value: 0	223.01+/-130.77 62.68+/-63.75 N1=40, N2=10 Fold Change: 3.85 P-value: .00019
585	1209	W80496	221.23+/-140.42 105.98+/-75.28 N1=40, N2=168 Fold Change: 2.11 P-value: 0	X	X	214.3+/-135.15 95.94+/-55.75 N1=40, N2=31 Fold Change: 2.13 P-value: .00004	214.3+/-135.15 53.76+/-58.28 N1=40, N2=10 Fold Change: 3.87 P-value: .00029
586	1211	W88427	669.14+/-243.38 316.73+/-233.88 N1=40, N2=168 Fold Change: 2.35 P-value: 0	X	X	661.21+/-241.27 304.22+/-202.92 N1=40, N2=31 Fold Change: 2.35 P-value: 0	661.21+/-241.27 187.14+/-59.43 N1=40, N2=10 Fold Change: 3.45 P-value: 0
587	1246	Z99386	615.03+/-208.26 262.6+/-122.89 N1=40, N2=168 Fold Change: 2.48 P-value: 0	X	X	611.71+/-209.91 245.54+/-120.4 N1=40, N2=31 Fold Change: 2.66 P-value: 0	611.71+/-209.91 231.83+/-120.93 N1=40, N2=10 Fold Change: 3.04 P-value: .00124

Table 5: BREAST / INFILTRATING LOBULAR CARCINOMA

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
1	7	AA017070	218.33+/-195.52 77.15+/-79.13 N1=40, N2=17 Fold Change: 2.53 P-value: .00187	X	X
2	15	AA031790	336.45+/-181.35 156.08+/-81.33 N1=40, N2=17 Fold Change: 2.16 P-value: .00003	X	X
3	23	AA044830	387.92+/-190.91 188.55+/-88.55 N1=40, N2=17 Fold Change: 2.14 P-value: .00023	X	X
4	24	AA045145	262.21+/-180.28 76.07+/-123.14 N1=40, N2=17 Fold Change: 3.26 P-value: .00038	X	X
5	25	AA046457	254.96+/-154.86 128.89+/-118.57 N1=40, N2=17 Fold Change: 2.3 P-value: .00176	X	X
6	31	AA059396	383.25+/-127.97 170.7+/-70.05 N1=40, N2=17 Fold Change: 2.32 P-value: 0	X	383.25+/-127.97 120.28+/-48.53 N1=40, N2=17 Fold Change: 3.22 P-value: .01218
7	33	AA059458	74.76+/-90.6 314.12+/-111.83 N1=40, N2=17 Fold Change: 5.79 P-value: 0	X	74.76+/-90.6 344.29+/-46.75 N1=40, N2=17 Fold Change: 6.82 P-value: 0
8	41	AA126704	312.64+/-137.34 130.96+/-82.96 N1=40, N2=17 Fold Change: 2.5 P-value: .00009	X	X
9	42	AA127718	240.21+/-361.64 75.73+/-121.03 N1=40, N2=17 Fold Change: 3.09 P-value: .00005	X	X
10	43	AA127727	212.97+/-123.48 100.07+/-53.82 N1=40, N2=17 Fold Change: 2.1 P-value: .00014	X	X
11	51	AA133248	400.91+/-134.73 201.52+/-119.8 N1=40, N2=17 Fold Change: 2.24 P-value: .00009	X	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
12	57	AA142913	302.34+/-222.83 104.53+/-62.4 N1=40, N2=17 Fold Change: 2.84 P-value: 0	X	302.34+/-222.83 68.29+/-31.77 N1=40, N2=17 Fold Change: 4.03 P-value: .00871
13	62	AA147751	478.2+/-207.42 245.52+/-144.78 N1=40, N2=17 Fold Change: 2.03 P-value: .00015	X	X
14	63	AA147884	46.86+/-55.16 212.3+/-151.24 N1=40, N2=17 Fold Change: 3.93 P-value: .00001	X	X
15	64	AA149312	374+/-139.43 179.7+/-77.1 N1=40, N2=17 Fold Change: 2.18 P-value: .00003	X	X
16	65	AA150501	215.8+/-104 97.75+/-48.53 N1=40, N2=17 Fold Change: 2.27 P-value: .00006	X	X
17	71	AA158731	287.72+/-241.22 94.76+/-99 N1=40, N2=17 Fold Change: 3.29 P-value: .00036	X	X
18	72	AA160156	630.23+/-274.77 297.85+/-166.73 N1=40, N2=17 Fold Change: 2.39 P-value: .00076	X	X
19	75	AA173572	368.73+/-173.58 140.6+/-66.1 N1=40, N2=17 Fold Change: 2.52 P-value: .00001	X	368.73+/-173.58 101.84+/-30.25 N1=40, N2=17 Fold Change: 3.17 P-value: .00053
20	84	AA203663	288.39+/-92.75 151.54+/-90.12 N1=40, N2=17 Fold Change: 2.19 P-value: .00062	X	X
21	88	AA227778	254.32+/-164.5 129.32+/-121.52 N1=40, N2=17 Fold Change: 2.21 P-value: .00551	X	X
22	99	AA369887	326.24+/-259.48 1569.71+/-1564.61 N1=40, N2=17 Fold Change: 3.13 P-value: .00723	X	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
23	117	AA430314	259.57+/-186.05 94.12+/-84.62 N1=40, N2=17 Fold Change: 2.81 P-value: .00057	X	259.57+/-186.05 51.43+/-32.49 N1=40, N2=17 Fold Change: 4.33 P-value: .0109
24	120	AA447015	226.67+/-173.74 86.47+/-87.06 N1=40, N2=17 Fold Change: 2.44 P-value: .00239	X	226.67+/-173.74 49.75+/-49 N1=40, N2=17 Fold Change: 3.69 P-value: .04932
25	121	AA448195	82.22+/-92.11 252.38+/-226.28 N1=40, N2=17 Fold Change: 2.56 P-value: .00561	X	X
26	122	AA450090	285.47+/-226.15 121.51+/-105.64 N1=40, N2=17 Fold Change: 2.56 P-value: .00017	X	285.47+/-226.15 80.74+/-67.6 N1=40, N2=17 Fold Change: 3.67 P-value: .04277
27	124	AA452295	220.36+/-116.43 43.55+/-34.23 N1=40, N2=17 Fold Change: 4.8 P-value: 0	X	220.36+/-116.43 27.93+/-7.95 N1=40, N2=17 Fold Change: 6.64 P-value: 0
28	129	AA479033	105.96+/-264.08 699.96+/-1244.37 N1=40, N2=17 Fold Change: 3.25 P-value: .01862	X	X
29	131	AA480075	331.5+/-159.34 170.51+/-174.22 N1=40, N2=17 Fold Change: 2.36 P-value: .00065	X	X
30	134	AA486731	417.18+/-216.76 258.38+/-279.38 N1=40, N2=17 Fold Change: 2.26 P-value: .0077	X	X
31	135	AA488889	298.86+/-194.94 114.61+/-41.42 N1=40, N2=17 Fold Change: 2.16 P-value: .00001	X	X
32	138	AA502943	439.24+/-110.96 200.97+/-110.89 N1=40, N2=17 Fold Change: 2.41 P-value: 0	X	X
33	140	AA508196	475.57+/-315.6 208.59+/-128.6 N1=40, N2=17 Fold Change: 2.29 P-value: .0014	X	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
34	142	AA516420	208.7+/-209.98 762.28+/-919.5 N1=40, N2=17 Fold Change: 2.83 P-value: .00199	X	X
35	151	AA526961	417.14+/-237.24 139.33+/-66.58 N1=40, N2=17 Fold Change: 2.89 P-value: 0	X	X
36	156	AA534456	1130.9+/-759.82 504.53+/-276.17 N1=40, N2=17 Fold Change: 2.23 P-value: .00282	X	X
37	160	AA535218	322.09+/-137.43 130.51+/-83.58 N1=40, N2=17 Fold Change: 2.69 P-value: .00001	X	X
38	171	AA584310	402.55+/-323.55 1185.08+/-725.81 N1=40, N2=17 Fold Change: 3.27 P-value: .00003	X	X
39	172	AA584403	593.26+/-1291.79 73.69+/-113.44 N1=40, N2=17 Fold Change: 3.63 P-value: .0001	X	593.26+/-1291.79 46.94+/-41.5 N1=40, N2=17 Fold Change: 4.08 P-value: .01967
40	175	AA601511	2941.11+/-4823.41 8196.8+/-10494.86 N1=40, N2=17 Fold Change: 3.59 P-value: .04627	X	X
41	178	AA609310	285.39+/-160.8 103.37+/-63.8 N1=40, N2=17 Fold Change: 2.73 P-value: .00003	X	X
42	180	AA610522	803+/-768.74 2236.91+/-2047.57 N1=40, N2=17 Fold Change: 3.15 P-value: .00504	X	803+/-768.74 1948.9+/-1536.5 N1=40, N2=17 Fold Change: 3.65 P-value: .04632
43	184	AA621478	398.69+/-325.12 105.85+/-99.55 N1=40, N2=17 Fold Change: 3.76 P-value: .00002	X	X
44	189	AA628467	1145.06+/-502.33 483.55+/-276.22 N1=40, N2=17 Fold Change: 2.59 P-value: .00016	X	1145.06+/-502.33 263.82+/-233.17 N1=40, N2=17 Fold Change: 5.48 P-value: .04561

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
45	191	AA631047	615.9+/-364.24 335.52+/-248.64 N1=40, N2=17 Fold Change: 2.12 P-value: .00214	X	X
46	194	AA634799	739.38+/-608.62 265.99+/-273.02 N1=40, N2=17 Fold Change: 3.37 P-value: .00153	X	X
47	198	AA669106	84.29+/-131.22 224.41+/-230.31 N1=40, N2=17 Fold Change: 3.18 P-value: .00001	X	X
48	200	AA700621	467.51+/-455.09 127.5+/-198.7 N1=40, N2=17 Fold Change: 3.36 P-value: .00047	X	467.51+/-455.09 65.41+/-73.63 N1=40, N2=17 Fold Change: 4.6 P-value: .03306
49	214	AA742697	1026.03+/-1071.41 497.89+/-1362.07 N1=40, N2=17 Fold Change: 3.28 P-value: .00238	X	1026.03+/-1071.41 72.76+/-23.65 N1=40, N2=17 Fold Change: 7.24 P-value: 0
50	253	AA921809	459.15+/-1266.29 1144.77+/-1121.05 N1=40, N2=17 Fold Change: 2.76 P-value: .00483	X	X
51	254	AA921830	92.93+/-115.1 214.98+/-154.53 N1=40, N2=17 Fold Change: 2.53 P-value: .00048	X	92.93+/-115.1 328.17+/-235.36 N1=40, N2=17 Fold Change: 4.07 P-value: .03148
52	255	AA921922	312.44+/-292.63 101.23+/-57.27 N1=40, N2=17 Fold Change: 2.73 P-value: .00001	X	312.44+/-292.63 79.08+/-33.3 N1=40, N2=17 Fold Change: 3.21 P-value: .00566
53	260	AA936632	X	X	125.03+/-127.3 341.96+/-182.6 N1=40, N2=17 Fold Change: 3.13 P-value: .02208
54	266	AA976064	363.9+/-153.14 150.7+/-67.67 N1=40, N2=17 Fold Change: 2.48 P-value: 0	X	X
55	281	AC004770	X	X	222.34+/-159.84 51.7+/-14.58 N1=40, N2=17 Fold Change: 3.51 P-value: .00008

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
56	**297**	**AF052142**	307.17+/-169.55 101.76+/-54.87 N1=40, N2=17 Fold Change: 2.92 P-value: 0	X	X
57	**317**	**AI018523**	422.08+/-187.64 137.17+/-133.59 N1=40, N2=17 Fold Change: 3.55 P-value: .00002	X	X
58	**321**	**AI031771**	85.9+/-105.07 273.11+/-256.97 N1=40, N2=17 Fold Change: 2.82 P-value: .00563	X	X
59	**324**	**AI039005**	203.54+/-131.69 79.78+/-68.07 N1=40, N2=17 Fold Change: 2.7 P-value: .00048	X	X
60	**325**	**AI039722**	X	X	1007.24+/-1162.59 71.46+/-83.95 N1=40, N2=17 Fold Change: 11.94 P-value: .00965
61	**331**	**AI057450**	381.32+/-1572.07 -3.82+/-29.02 N1=40, N2=17 Fold Change: 3.3 P-value: .00001	X	381.32+/-1572.07 -11.17+/-8.38 N1=40, N2=17 Fold Change: 3.63 P-value: 0
62	**333**	**AI073394**	124.23+/-101.36 255.64+/-158.11 N1=40, N2=17 Fold Change: 2.2 P-value: .00025	X	X
63	**335**	**AI073992**	110.23+/-145.3 533.62+/-785.24 N1=40, N2=17 Fold Change: 3.22 P-value: .00574	X	X
64	**338**	**AI079545**	248.94+/-138.38 465.02+/-171.05 N1=40, N2=17 Fold Change: 2.01 P-value: .00007	X	X
65	**341**	**AI083598**	339.56+/-289.33 75.11+/-72.52 N1=40, N2=17 Fold Change: 3.79 P-value: .00003	X	339.56+/-289.33 38.38+/-30.41 N1=40, N2=17 Fold Change: 5.72 P-value: .00274
66	**342**	**AI086614**	301.2+/-152.86 128.33+/-84.7 N1=40, N2=17 Fold Change: 2.51 P-value: .00041	X	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
67	343	AI087975	68.87+/-58.02 211.46+/-250.57 N1=40, N2=17 Fold Change: 2.28 P-value: .00976	X	X
68	344	AI088609	709.25+/-600.21 265.96+/-356.75 N1=40, N2=17 Fold Change: 3.21 P-value: .00094	X	X
69	345	AI091154	351.29+/-406.17 74.97+/-110.43 N1=40, N2=17 Fold Change: 4.1 P-value: .00011	X	351.29+/-406.17 12.49+/-5.56 N1=40, N2=17 Fold Change: 8.99 P-value: 0
70	351	AI123555	300+/-164.6 65.25+/-46.06 N1=40, N2=17 Fold Change: 4.55 P-value: 0	X	300+/-164.6 48.57+/-47.56 N1=40, N2=17 Fold Change: 6 P-value: .01993
71	359	AI128820	224.42+/-90.96 108.28+/-86.45 N1=40, N2=17 Fold Change: 2.34 P-value: .00033	X	X
72	361	AI129626	278.92+/-134.16 134.17+/-77.75 N1=40, N2=17 Fold Change: 2.13 P-value: .00023	X	X
73	362	AI131078	299.48+/-223.81 111.16+/-71.9 N1=40, N2=17 Fold Change: 2.6 P-value: .0002	X	299.48+/-223.81 67.7+/-89.93 N1=40, N2=17 Fold Change: 5.06 P-value: .04594
74	370	AI148006	241.17+/-193.5 77.61+/-92.82 N1=40, N2=17 Fold Change: 2.93 P-value: .00043	X	X
75	372	AI149637	212.6+/-241.64 39.92+/-27.3 N1=40, N2=17 Fold Change: 3.37 P-value: 0	X	212.6+/-241.64 39.29+/-41.66 N1=40, N2=17 Fold Change: 3.31 P-value: .04204
76	380	AI189011	284.7+/-101.6 126.14+/-81.81 N1=40, N2=17 Fold Change: 2.75 P-value: .00017	X	X
77	384	AI200954	524.84+/-319.36 253.81+/-173.45 N1=40, N2=17 Fold Change: 2.17 P-value: .00291	X	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
78	386	AI201965	X	X	234.24+/-149.37 59.16+/-44.89 N1=40, N2=17 Fold Change: 3.61 P-value: .03602
79	394	AI222594	431.73+/-162.38 196.71+/-138.58 N1=40, N2=17 Fold Change: 2.48 P-value: .00005	X	X
80	395	AI223817	221.5+/-204.3 686.72+/-465.96 N1=40, N2=17 Fold Change: 3.28 P-value: .00041	X	X
81	399	AI247837	250.33+/-314.52 53.27+/-43.26 N1=40, N2=17 Fold Change: 2.95 P-value: .00014	X	250.33+/-314.52 28.03+/-28.56 N1=40, N2=17 Fold Change: 4.49 P-value: .00427
82	408	AI277612	1022.91+/-907.07 101.24+/-106.96 N1=40, N2=17 Fold Change: 8.06 P-value: 0	X	387.19+/-203.85 584.56+/-51.28 N1=40, N2=17 Fold Change: 2.01 P-value: .00012
83	417	AI300876	601.83+/-985.51 26.36+/-32.43 N1=40, N2=17 Fold Change: 7.1 P-value: 0	X	601.83+/-985.51 28.36+/-46.5 N1=40, N2=17 Fold Change: 6.7 P-value: .00688
84	418	AI301060	1095.7+/-461.79 3285.81+/-2230.69 N1=40, N2=17 Fold Change: 2.58 P-value: .00018	X	X
85	422	AI333767	201.68+/-104.32 94.33+/-75 N1=40, N2=17 Fold Change: 2.32 P-value: .00023	X	X
86	423	AI333987	X	X	208.53+/-320.79 -12.06+/-45.78 N1=40, N2=17 Fold Change: 4.29 P-value: .00037
87	427	AI341602	137.44+/-280.1 473.63+/-503.04 N1=40, N2=17 Fold Change: 3.72 P-value: .00123	X	137.44+/-280.1 1084.1+/-558.85 N1=40, N2=17 Fold Change: 14.07 P-value: .00013
88	430	AI344312	85.72+/-58.03 241.24+/-132.01 N1=40, N2=17 Fold Change: 2.77 P-value: .00003	X	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
89	**431**	**AI346341**	635.18+/-426.52 192.7+/-146.21 N1=40, N2=17 Fold Change: 2.74 P-value: .00095	X	X
90	**442**	**AI369840**	239.87+/-167.43 91.16+/-73.21 N1=40, N2=17 Fold Change: 2.54 P-value: .00091	X	X
91	**447**	**AI378584**	815.22+/-371.96 289.2+/-132.28 N1=40, N2=17 Fold Change: 2.65 P-value: 0	X	815.22+/-371.96 225.35+/-105.83 N1=40, N2=17 Fold Change: 3.53 P-value: .02945
92	**448**	**AI379723**	380.22+/-173.64 171.75+/-85.82 N1=40, N2=17 Fold Change: 2.11 P-value: .00049	X	X
93	**459**	**AI394013**	X	X	81.65+/-57.28 206.8+/-28.72 N1=40, N2=17 Fold Change: 3.01 P-value: 0
94	**462**	**AI417267**	933.35+/-487.41 367.83+/-178.5 N1=40, N2=17 Fold Change: 2.35 P-value: 0	X	933.35+/-487.41 232.02+/-44.3 N1=40, N2=17 Fold Change: 3.44 P-value: 0
95	**467**	**AI419030**	445.97+/-259.12 141.54+/-110.04 N1=40, N2=17 Fold Change: 3.4 P-value: .00002	X	445.97+/-259.12 100.89+/-50.85 N1=40, N2=17 Fold Change: 3.94 P-value: .00968
96	**468**	**AI421837**	293.96+/-147.73 122.58+/-60.8 N1=40, N2=17 Fold Change: 2.25 P-value: .00003	X	X
97	**477**	**AI458003**	280.16+/-202.76 58.35+/-64.44 N1=40, N2=17 Fold Change: 4.09 P-value: 0	X	280.16+/-202.76 29.02+/-54.63 N1=40, N2=17 Fold Change: 6.1 P-value: .01261
98	**484**	**AI479262**	56.35+/-67.19 253.01+/-258.86 N1=40, N2=17 Fold Change: 3.34 P-value: .00113	X	X
99	**489**	**AI492051**	382.34+/-177.78 99.97+/-58.1 N1=40, N2=17 Fold Change: 3.83 P-value: 0	X	382.34+/-177.78 84.79+/-58.36 N1=40, N2=17 Fold Change: 4.59 P-value: .01274

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
100	**493**	**AI492879**	219.42+/-658.12 360.39+/-664.73 N1=40, N2=17 Fold Change: 3.18 P-value: .00218	X	X
101	**500**	**AI524085**	388.89+/-529.52 77.76+/-117.23 N1=40, N2=17 Fold Change: 3.83 P-value: .00013	X	X
102	**501**	**AI525044**	316.89+/-143.08 163.75+/-85.16 N1=40, N2=17 Fold Change: 2.13 P-value: .00114	X	X
103	**505**	**AI537407**	278.8+/-204.74 783.29+/-533.91 N1=40, N2=17 Fold Change: 2.81 P-value: .00083	X	X
104	**506**	**AI539386**	1924.9+/-2430.34 6121.55+/-7013.05 N1=40, N2=17 Fold Change: 3.2 P-value: .00044	X	X
105	**511**	**AI554514**	90.74+/-52.8 201.02+/-166.43 N1=40, N2=17 Fold Change: 2.08 P-value: .00026	X	X
106	**512**	**AI557210**	129.15+/-140.98 491.52+/-264.84 N1=40, N2=17 Fold Change: 5.08 P-value: 0	X	129.15+/-140.98 573+/-162.6 N1=40, N2=17 Fold Change: 6.68 P-value: .00001
107	**517**	**AI566038**	257.62+/-109.32 124.43+/-63.25 N1=40, N2=17 Fold Change: 2.16 P-value: .00015	X	X
108	**520**	**AI571525**	265.11+/-78.71 141.93+/-62.73 N1=40, N2=17 Fold Change: 2.04 P-value: .00015	X	X
109	**536**	**AI624853**	373.05+/-166.36 180.19+/-106.47 N1=40, N2=17 Fold Change: 2.21 P-value: .00004	X	X
110	**540**	**AI634852**	278.07+/-162.92 122.35+/-122.97 N1=40, N2=17 Fold Change: 2.6 P-value: .00095	X	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
111	542	AI638295	X	X	220.74+/-876.87 3.1+/-10.99 N1=40, N2=17 Fold Change: 3.16 P-value: 0
112	545	AI650341	123.6+/-154.23 209.61+/-97.49 N1=40, N2=17 Fold Change: 2.41 P-value: .00028	X	X
113	546	AI650514	110.57+/-163.5 295.11+/-242 N1=40, N2=17 Fold Change: 2.56 P-value: .00744	X	X
114	562	AI658925	542.56+/-347.67 259.65+/-161.58 N1=40, N2=17 Fold Change: 2.07 P-value: .00351	X	X
115	565	AI659418	261.02+/-116.11 133.75+/-108.49 N1=40, N2=17 Fold Change: 2.41 P-value: .00088	X	X
116	566	AI659533	563.4+/-201.34 291.04+/-136.51 N1=40, N2=17 Fold Change: 2.1 P-value: .00023	X	X
117	588	AI680541	510.08+/-201.29 186.08+/-102.82 N1=40, N2=17 Fold Change: 2.84 P-value: 0	X	510.08+/-201.29 106.49+/-44.75 N1=40, N2=17 Fold Change: 4.54 P-value: .00246
118	591	AI683911	241.46+/-200.89 27.24+/-52.93 N1=40, N2=17 Fold Change: 4.58 P-value: 0	X	241.46+/-200.89 32.69+/-57.65 N1=40, N2=17 Fold Change: 3.74 P-value: .01617
119	592	AI684457	96.99+/-74.31 253.71+/-245.09 N1=40, N2=17 Fold Change: 2.25 P-value: .00425	X	X
120	593	AI686114	374.48+/-274.59 120.83+/-92.86 N1=40, N2=17 Fold Change: 3.03 P-value: .0001	X	374.48+/-274.59 76.06+/-83.42 N1=40, N2=17 Fold Change: 4.43 P-value: .04695
121	612	AI701034	215.78+/-96.65 111.85+/-71.77 N1=40, N2=17 Fold Change: 2.11 P-value: .00036	X	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
122	618	AI732274	947.08+/-989.69 285.99+/-458.46 N1=40, N2=17 Fold Change: 3.94 P-value: .00251	X	X
123	619	AI733679	325.9+/-596.22 48.5+/-33.81 N1=40, N2=17 Fold Change: 3.21 P-value: .00002	X	X
124	623	AI740621	231.84+/-247.13 77.35+/-124.9 N1=40, N2=17 Fold Change: 2.62 P-value: .00315	X	X
125	627	AI742002	111.78+/-132.43 379.6+/-168.26 N1=40, N2=17 Fold Change: 4.61 P-value: 0	X	111.78+/-132.43 388+/-292.79 N1=40, N2=17 Fold Change: 4.32 P-value: .0111
126	629	AI742239	159.76+/-199.32 419.47+/-377.4 N1=40, N2=17 Fold Change: 3.29 P-value: .00013	X	X
127	631	AI742490	601.57+/-252.84 285.13+/-140.07 N1=40, N2=17 Fold Change: 2.05 P-value: .00003	X	X
128	632	AI742521	215.93+/-234.91 23.91+/-22.33 N1=40, N2=17 Fold Change: 4.4 P-value: 0	X	215.93+/-234.91 23.3+/-12.66 N1=40, N2=17 Fold Change: 4.76 P-value: .00002
129	635	AI743671	582.82+/-317.91 281.49+/-185.49 N1=40, N2=17 Fold Change: 2.26 P-value: .00964	X	X
130	636	AI743715	312.02+/-238.55 99.48+/-141.4 N1=40, N2=17 Fold Change: 3.47 P-value: .0005	X	X
131	637	AI743925	663.58+/-309.38 221.31+/-142.28 N1=40, N2=17 Fold Change: 3.13 P-value: 0	X	X
132	641	AI751438	144.67+/-188.73 551.05+/-364.64 N1=40, N2=17 Fold Change: 4.85 P-value: 0	X	144.67+/-188.73 612.92+/-347.94 N1=40, N2=17 Fold Change: 5.61 P-value: .02877

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
133	643	AI758223	833.52+/-665.83 89.52+/-74.43 N1=40, N2=17 Fold Change: 8.3 P-value: 0	X	833.52+/-665.83 98.81+/-90.66 N1=40, N2=17 Fold Change: 8 P-value: .02464
134	649	AI761241	883.3+/-332.12 415.64+/-208.2 N1=40, N2=17 Fold Change: 2.21 P-value: .00005	X	X
135	650	AI761274	342.36+/-182.65 121.18+/-64.61 N1=40, N2=17 Fold Change: 2.86 P-value: .00001	X	342.36+/-182.65 75.25+/-39.87 N1=40, N2=17 Fold Change: 4.5 P-value: .01949
136	652	AI761844	278.83+/-138.41 99.54+/-56.16 N1=40, N2=17 Fold Change: 2.79 P-value: .00001	X	278.83+/-138.41 87.16+/-56.51 N1=40, N2=17 Fold Change: 3.1 P-value: .02791
137	653	AI763136	282.1+/-149.81 118.7+/-131.83 N1=40, N2=17 Fold Change: 2.53 P-value: .00163	X	X
138	655	AI766029	271.74+/-528.19 22.11+/-18.39 N1=40, N2=17 Fold Change: 3.71 P-value: 0	X	271.74+/-528.19 30.31+/-29.22 N1=40, N2=17 Fold Change: 3.07 P-value: .01978
139	657	AI768325	114.7+/-66.43 257.51+/-172.22 N1=40, N2=17 Fold Change: 2.12 P-value: .00044	X	X
140	664	AI791182	286.48+/-162.61 621.07+/-388.18 N1=40, N2=17 Fold Change: 2.07 P-value: .00052	X	X
141	668	AI792635	X	X	800.24+/-717.81 1968.88+/-866 N1=40, N2=17 Fold Change: 4.27 P-value: .0038
142	674	AI797276	271.48+/-136.73 106.25+/-58.1 N1=40, N2=17 Fold Change: 2.56 P-value: .00001	X	271.48+/-136.73 76.49+/-46.61 N1=40, N2=17 Fold Change: 3.58 P-value: .02759
143	678	AI799784	603.99+/-383.42 93.05+/-88.68 N1=40, N2=17 Fold Change: 6.66 P-value: 0	X	603.99+/-383.42 82.71+/-78.29 N1=40, N2=17 Fold Change: 7.34 P-value: .01379

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
144	684	AI804054	302.97+/-234.41 108.18+/-91.04 N1=40, N2=17 Fold Change: 2.83 P-value: .00011	X	302.97+/-234.41 77.58+/-36.68 N1=40, N2=17 Fold Change: 3.3 P-value: .01862
145	687	AI806324	211.46+/-131.17 108.84+/-79.43 N1=40, N2=17 Fold Change: 2.03 P-value: .00874	X	X
146	691	AI809953	383.43+/-189.32 120.52+/-100.18 N1=40, N2=17 Fold Change: 3.27 P-value: .00013	X	X
147	693	AI810266	68.88+/-106.64 761.49+/-1126.65 N1=40, N2=17 Fold Change: 6.3 P-value: .00013	X	X
148	694	AI810764	202.16+/-159.83 1084.09+/-1401.59 N1=40, N2=17 Fold Change: 4.41 P-value: .00007	X	X
149	701	AI816835	360.85+/-289.77 171.05+/-158.66 N1=40, N2=17 Fold Change: 2.13 P-value: .00229	X	X
150	704	AI817967	X	X	112.71+/-118.41 308.86+/-160.78 N1=40, N2=17 Fold Change: 3.45 P-value: .00951
151	706	AI818579	394.08+/-228.07 204.91+/-197.94 N1=40, N2=17 Fold Change: 2.13 P-value: .00391	X	X
152	712	AI821472	519.11+/-694.13 -5.59+/-218.89 N1=40, N2=17 Fold Change: 5.69 P-value: .00005	X	519.11+/-694.13 -49.74+/-70.96 N1=40, N2=17 Fold Change: 9.33 P-value: 0
153	713	AI823572	232.21+/-195.63 91.57+/-60.62 N1=40, N2=17 Fold Change: 2.43 P-value: .00008	X	X
154	721	AI825936	229.86+/-148.12 98.58+/-81.47 N1=40, N2=17 Fold Change: 2.58 P-value: .00016	X	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
155	**722**	**AI826437**	45.86+/-118.99 281.35+/-448.25 N1=40, N2=17 Fold Change: 3.03 P-value: .0122	X	X
156	**744**	**AI863167**	183.76+/-73.48 406.96+/-190.24 N1=40, N2=17 Fold Change: 2.16 P-value: 0	X	X
157	**747**	**AI864898**	401.86+/-258.51 75.46+/-68.5 N1=40, N2=17 Fold Change: 5.61 P-value: 0	X	X
158	**750**	**AI871044**	766.39+/-500.99 189.5+/-179.55 N1=40, N2=17 Fold Change: 4.03 P-value: .00001	X	766.39+/-500.99 84.85+/-70.19 N1=40, N2=17 Fold Change: 8.12 P-value: .00884
159	**751**	**AI872267**	267.23+/-203.1 627.26+/-368.25 N1=40, N2=17 Fold Change: 2.55 P-value: .00015	X	X
160	**752**	**AI879337**	431.51+/-184.18 215.5+/-115.86 N1=40, N2=17 Fold Change: 2.18 P-value: .00062	X	X
161	**758**	**AI888322**	X	X	319.22+/-320.74 71.54+/-51.15 N1=40, N2=17 Fold Change: 3.78 P-value: .03277
162	**772**	**AI916544**	151.27+/-163.24 373.43+/-334.2 N1=40, N2=17 Fold Change: 2.45 P-value: .00524	X	X
163	**775**	**AI917901**	601.53+/-812.45 76.98+/-131.25 N1=40, N2=17 Fold Change: 4.95 P-value: .00005	X	601.53+/-812.45 26.66+/-20.01 N1=40, N2=17 Fold Change: 7.3 P-value: .00001
164	**780**	**AI924465**	448.27+/-478.27 149.48+/-115.97 N1=40, N2=17 Fold Change: 2.43 P-value: .00214	X	X
165	**787**	**AI934361**	220.01+/-243.16 54.43+/-44.52 N1=40, N2=17 Fold Change: 3.1 P-value: .00001	X	220.01+/-243.16 52.02+/-37.1 N1=40, N2=17 Fold Change: 3.01 P-value: .03711

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
166	**789**	**AI934881**	316.72+/-226.37 659.59+/-486.96 N1=40, N2=17 Fold Change: 2.01 P-value: .00378	X	X
167	**816**	**AI968151**	127.39+/-61.78 376.92+/-292.97 N1=40, N2=17 Fold Change: 2.53 P-value: .00031	X	X
168	**817**	**AI968379**	295.46+/-388.02 -8.49+/-25.52 N1=40, N2=17 Fold Change: 6.27 P-value: 0	X	295.46+/-388.02 .59+/-34.6 N1=40, N2=17 Fold Change: 5.43 P-value: .00032
169	**818**	**AI968904**	738.79+/-292.65 307.62+/-119.37 N1=40, N2=17 Fold Change: 2.35 P-value: 0	X	X
170	**830**	**AI972498**	286.51+/-112.64 135.46+/-66.44 N1=40, N2=17 Fold Change: 2.18 P-value: .00003	X	X
171	**832**	**AI972873**	436.16+/-215 132.01+/-99.1 N1=40, N2=17 Fold Change: 3.85 P-value: 0	X	X
172	**838**	**AI983045**	281.02+/-338.08 40.45+/-125.75 N1=40, N2=17 Fold Change: 4.78 P-value: 0	X	281.02+/-338.08 -9.19+/-15.96 N1=40, N2=17 Fold Change: 7.52 P-value: 0
173	**857**	**AL037805**	X	X	614.2+/-317.15 183.89+/-87.99 N1=40, N2=17 Fold Change: 3.13 P-value: .01435
174	**865**	**AL040912**	304.56+/-132.78 112.19+/-70.33 N1=40, N2=17 Fold Change: 2.8 P-value: .00006	X	X
175	**867**	**AL042492**	809.69+/-853.09 72.75+/-93.44 N1=40, N2=17 Fold Change: 9.48 P-value: 0	X	1022.91+/-907.07 85.76+/-67.41 N1=40, N2=17 Fold Change: 8.09 P-value: .00176
176	**876**	**AL046941**	428.58+/-238.89 146.79+/-176.57 N1=40, N2=17 Fold Change: 4.06 P-value: .00007	X	428.58+/-238.89 55.32+/-48.1 N1=40, N2=17 Fold Change: 7.58 P-value: .01267

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
177	881	AL048962	944+/-354.29 399.3+/-211.63 N1=40, N2=17 Fold Change: 2.5 P-value: .00001	X	944+/-354.29 289.62+/-184.81 N1=40, N2=17 Fold Change: 3.52 P-value: .03411
178	893	AL050367	257.59+/-77.75 111.77+/-59.21 N1=40, N2=17 Fold Change: 2.47 P-value: 0	X	257.59+/-77.75 76.12+/-36.74 N1=40, N2=17 Fold Change: 3.45 P-value: .01201
179	894	AL079279	313.49+/-189.76 127.56+/-77.14 N1=40, N2=17 Fold Change: 2.4 P-value: .00036	X	X
180	896	AL079707	261.69+/-226.08 73.98+/-35.27 N1=40, N2=17 Fold Change: 3.16 P-value: 0	X	X
181	902	AL118746	234.63+/-113.05 84.77+/-47.29 N1=40, N2=17 Fold Change: 2.86 P-value: .00001	X	234.63+/-113.05 46.19+/-34.43 N1=40, N2=17 Fold Change: 5.14 P-value: .0179
182	905	AW000952	98.9+/-72.25 204.67+/-105.21 N1=40, N2=17 Fold Change: 2.16 P-value: .00011	X	X
183	907	AW002846	283.14+/-201.6 119.62+/-87.38 N1=40, N2=17 Fold Change: 2.43 P-value: .00065	X	X
184	908	AW002941	959.64+/-342.08 493.25+/-243.21 N1=40, N2=17 Fold Change: 2.13 P-value: .0001	X	X
185	916	AW006235	346.9+/-210.26 121.01+/-58.03 N1=40, N2=17 Fold Change: 2.69 P-value: 0	X	X
186	917	AW006352	235.29+/-179.11 534.97+/-420.56 N1=40, N2=17 Fold Change: 2.17 P-value: .00953	X	X
187	921	AW007080	223.2+/-116.87 69.24+/-50.48 N1=40, N2=17 Fold Change: 3.27 P-value: .00001	X	223.2+/-116.87 36.39+/-14.01 N1=40, N2=17 Fold Change: 5.16 P-value: .0001

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
188	926	AW007803	153.39+/-142.06 442.5+/-397.54 N1=40, N2=17 Fold Change: 2.55 P-value: .00867	X	X
189	931	AW014155	214.48+/-209.56 624.36+/-372.34 N1=40, N2=17 Fold Change: 3.15 P-value: .00005	X	X
190	953	AW051492	442.65+/-332.99 203.39+/-140.38 N1=40, N2=17 Fold Change: 2.22 P-value: .00151	X	X
191	957	C17781	229.36+/-141.71 84.23+/-69.19 N1=40, N2=17 Fold Change: 2.59 P-value: .00012	X	X
192	975	F22640	416.82+/-153.5 204.94+/-169.19 N1=40, N2=17 Fold Change: 2.37 P-value: .00007	X	X
193	985	H16568	288.53+/-212.27 74.99+/-76.74 N1=40, N2=17 Fold Change: 3.32 P-value: .00019	X	288.53+/-212.27 32.47+/-46.57 N1=40, N2=17 Fold Change: 5.01 P-value: .01332
194	988	H30384	194.93+/-133.51 479.18+/-480.95 N1=40, N2=17 Fold Change: 2.18 P-value: .00329	X	X
195	992	H54254	377.04+/-687.01 38.27+/-23.01 N1=40, N2=17 Fold Change: 4.25 P-value: 0	X	377.04+/-687.01 36.82+/-32.95 N1=40, N2=17 Fold Change: 4.51 P-value: .00966
196	997	H92988	390.91+/-149.13 205.04+/-140.06 N1=40, N2=17 Fold Change: 2.33 P-value: .00168	X	X
197	1074	N42752	63.77+/-48.02 291.54+/-224.99 N1=40, N2=17 Fold Change: 3.86 P-value: .00006	X	X
198	1085	N56877	109.5+/-80.79 402.12+/-388.61 N1=40, N2=17 Fold Change: 3 P-value: .00087	X	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
199	**1090**	**N63913**	458.01+/-316.71 67.39+/-79.5 N1=40, N2=17 Fold Change: 6.57 P-value: 0	X	458.01+/-316.71 8.79+/-40.55 N1=40, N2=17 Fold Change: 11.59 P-value: .00004
200	**1101**	**R08000**	502.76+/-694.51 82.03+/-53.39 N1=40, N2=17 Fold Change: 3.78 P-value: 0	X	502.76+/-694.51 90.53+/-93.25 N1=40, N2=17 Fold Change: 4.05 P-value: .04964
201	**1104**	**R20784**	1112.78+/-843.96 359.34+/-233.36 N1=40, N2=17 Fold Change: 2.91 P-value: .00005	X	X
202	**1105**	**R39938**	111.89+/-67.41 222.22+/-111.16 N1=40, N2=17 Fold Change: 2.12 P-value: .00002	X	X
203	**1106**	**R42575**	90.17+/-38.15 215.36+/-156.29 N1=40, N2=17 Fold Change: 2.01 P-value: .00211	X	X
204	**1112**	**R54660**	200.26+/-133.86 48.69+/-33.36 N1=40, N2=17 Fold Change: 3.43 P-value: 0	X	200.26+/-133.86 29.39+/-27.33 N1=40, N2=17 Fold Change: 4.69 P-value: .0025
205	**1116**	**R70255**	241.29+/-181.34 14.29+/-38.71 N1=40, N2=17 Fold Change: 5.79 P-value: 0	X	241.29+/-181.34 -8.34+/-15.47 N1=40, N2=17 Fold Change: 7.98 P-value: 0
206	**1118**	**R74561**	425.23+/-350.96 879.43+/-654.71 N1=40, N2=17 Fold Change: 2.16 P-value: .0019	X	X
207	**1119**	**R83604**	304.76+/-867.74 -32.63+/-64.18 N1=40, N2=17 Fold Change: 3.15 P-value: .00017	X	X
208	**1125**	**T61106**	180.38+/-114.3 349.03+/-164.74 N1=40, N2=17 Fold Change: 2.35 P-value: .00001	X	X
209	**1132**	**T85314**	X	X	166.2+/-116.99 644.58+/-401.95 N1=40, N2=17 Fold Change: 4.09 P-value: .03546

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
210	**1171**	**W02823**	217.4+/-87.18 81.39+/-47.18 N1=40, N2=17 Fold Change: 2.83 P-value: .00001	X	217.4+/-87.18 53.69+/-25.71 N1=40, N2=17 Fold Change: 3.92 P-value: .00806
211	**1173**	**W07043**	299.21+/-164.12 105.66+/-83.76 N1=40, N2=17 Fold Change: 2.82 P-value: .00008	X	299.21+/-164.12 59.94+/-40.54 N1=40, N2=17 Fold Change: 4.46 P-value: .01951
212	**1174**	**W07304**	1139.71+/-444.58 502.93+/-458.99 N1=40, N2=17 Fold Change: 2.64 P-value: .00012	X	1139.71+/-444.58 349.93+/-213.71 N1=40, N2=17 Fold Change: 3.49 P-value: .04978
213	**1180**	**W27541**	X	X	486.94+/-189.31 113.57+/-41.71 N1=40, N2=17 Fold Change: 4.17 P-value: .0025
214	**1183**	**W32480**	720.17+/-951.89 76.05+/-158.18 N1=40, N2=17 Fold Change: 7.94 P-value: 0	X	720.17+/-951.89 18.91+/-12.14 N1=40, N2=17 Fold Change: 12.97 P-value: 0
215	**1184**	**W37770**	208.87+/-62 108.93+/-55.29 N1=40, N2=17 Fold Change: 2.1 P-value: .00006	X	X
216	**1185**	**W37896**	499.73+/-192.2 1636.96+/-1336.48 N1=40, N2=17 Fold Change: 2.49 P-value: .00074	X	X
217	**1198**	**W72338**	464.08+/-121.49 964.48+/-427.69 N1=40, N2=17 Fold Change: 2 P-value: 0	X	X
218	**1199**	**W72347**	368.08+/-157.32 134.9+/-113.13 N1=40, N2=17 Fold Change: 3.01 P-value: .00008	X	X
219	**1200**	**W72407**	234.77+/-159.7 50.76+/-52.77 N1=40, N2=17 Fold Change: 4.25 P-value: 0	X	234.77+/-159.7 44.31+/-63.03 N1=40, N2=17 Fold Change: 5.12 P-value: .03464
220	**1201**	**W72511**	988.5+/-437.53 477.34+/-271.59 N1=40, N2=17 Fold Change: 2.11 P-value: .00006	X	X

#	Seq ID	Genbank	Normal vs All	Normal vs Malignant	Normal vs SII and SIII
221	**1204**	**W73386**	248.29+/-403.35 35.26+/-68.97 N1=40, N2=17 Fold Change: 3.18 P-value: .0001	469.37+/-905.14 101.34+/-51.41 N1=17, N2=7 Fold Change: 2.82 P-value: .01061	X
222	**1207**	**W73890**	223.01+/-130.77 84.82+/-49.32 N1=40, N2=17 Fold Change: 2.49 P-value: 0	X	X
223	**1246**	**Z99386**	611.71+/-209.91 288.23+/-106.96 N1=40, N2=17 Fold Change: 2.19 P-value: .00001	X	X

What is claimed is:

1. A method of diagnosing breast cancer in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 1-5; wherein differential expression of the genes in Tables 1-5 is indicative of breast cancer.

2. A method of detecting the progression of breast cancer in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 1-5; wherein differential expression of the genes in Tables 1-5 is indicative of breast cancer progression.

3. A method of monitoring the treatment of a patient with breast cancer, comprising:

(a) administering a pharmaceutical composition to the patient;

(b) preparing a gene expression profile from a cell or tissue sample from the patient; and

(c) comparing the patient gene expression profile to a gene expression from a cell population selected from the group consisting of normal breast cells and cancerous breast cells.

4. A method of treating a patient with breast cancer, comprising:

(a) administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 1-5;

(b) preparing a gene expression profile from a cell or tissue sample from the patient comprising tumor cells; and

(c) comparing the patient expression profile to a gene expression profile selected from the group consisting of normal breast cells and cancerous breast cells.

5. A method of typing breast cancer in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 1-5; wherein differential expression of the genes in Tables 1-5 is indicative of a type of breast cancer selected from a group consisting of infiltrating ductal carcinoma, microinvasive carcinoma, cribiform carcinoma, stage I carcinoma, stage II carcinoma, stage III carcinoma or lobular carcinoma.

6. A method of detecting the presence or progression of infiltrating ductal carcinoma in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 1-5; wherein differential expression of the genes in Tables 1-5 is indicative of infiltrating ductal carcinoma progression.

7. A method of monitoring the treatment of a patient with infiltrating ductal carcinoma, comprising:

(a) administering a pharmaceutical composition to the patient;

(b) preparing a gene expression profile from a cell or tissue sample from the patient; and

(c) comparing the patient gene expression profile to a gene expression from a cell population comprising normal breast cells or to a gene expression profile from a cell population comprising infiltrating ductal carcinoma cells or to both.

8. A method of treating a patient with infiltrating ductal carcinoma, comprising:

(a) administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 1-5;

(b) preparing a gene expression profile from a cell or tissue sample from the patient comprising infiltrating ductal carcinoma cells; and

(c) comparing the patient expression profile to a gene expression profile from an untreated cell population comprising infiltrating ductal carcinoma cells.

9. A method of diagnosing a microinvasive form of breast tumor in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 1-5; wherein differential expression of the genes in Tables 1-5 is indicative of a microinvasive form of breast cancer.

10. A method of detecting the progression of a microinvasive for of breast cancer in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 1-5; wherein differential expression of the genes in Tables 1-5 is indicative of the progression of a microinvasive form of breast cancer.

11. A method of monitoring the treatment of a patient with a microinvasive form of breast cancer, comprising:

(a) administering a pharmaceutical composition to the patient;

(b) preparing a gene expression profile from a cell or tissue sample from the patient; and

(c) comparing the patient gene expression profile to a gene expression from a cell population comprising normal breast cells or to a gene expression profile from a cell population comprising microinvasive breast cancer cells or to both.

12. A method of treating a patient with a microinvasive form of breast cancer, comprising:

(a) administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 1-5;

(b) preparing a gene expression profile from a cell or tissue sample from the patient comprising microinvasive breast cancer cells; and

(c) comparing the patient expression profile to a gene expression profile from an untreated cell population comprising microinvasive breast cancer cells.

13. A method of differentiating microinvasive breast cancer from a benign growth in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 1-5; wherein differential expression of the genes in Tables 1-5 is indicative of microinvasive breast cancer rather than benign growth.

14. A method of screening for an agent capable of modulating the onset or progression of breast cancer, comprising:

(a) preparing a first gene expression profile of a cell population comprising breast cancer cells, wherein the expression profile determines the expression level of one or more genes from Tables 1-5;

(b) exposing the cell population to the agent;

(c) preparing second gene expression profile of the agent-exposed cell population; and

(d) comparing the first and second gene expression profiles.

15. The method of claim 14, wherein the breast cancer is a infiltrating ductal carcinoma.

16. The method of claim 14, wherein the breast cancer is a microinvasive breast cancer.

17. A composition comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 1-5.

18. A composition according to claim 17, wherein the composition comprises at least 3 oligonucleotides.

19. A composition according to claim 17, wherein the composition comprises at least 5 oligonucleotides.

20. A composition according to claim 17, wherein the composition comprises at least 7 oligonucleotides.

21. A composition according to claim 17, wherein the composition comprises at least 10 oligonucleotides.

22. A composition according to any one of claims 17-21, wherein the oligonucleotides are attached to a solid support.

23. A composition according to claim 22, wherein the solid support is selected from a group consisting of a membrane, a glass support, a filter, a tissue culture dish, a polymeric material, a bead and a silica support.

24. A solid support comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 1-5.

25. A solid support according to claim 24, wherein the oligonucleotides are covalently attached to the solid support.

26. A solid support according to claim 24, wherein the oligonucleotides are non-covalently attached to the solid support.

27. A solid support according to claim 24, wherein the support comprises at least about 10 different oligonucleotides in discrete locations per square centimeter.

28. A solid support according to claim 24, wherein the support comprises at least about 100 different oligonucleotides in discrete locations per square centimeter.

29. A solid support according to claim 24, wherein the support comprises at least about 1000 different oligonucleotides in discrete locations per square centimeter.

30. A solid support according to claim 24, wherein the support comprises at least about 10,000 different oligonucleotides in discrete locations per square centimeter.

31. A computer system comprising:

(a) a database containing information identifying the expression level in breast tissue of a set of genes comprising at least two genes in Tables 1-5; and

(b) a user interface to view the information.

32. A computer system of claim 31, wherein the database further comprises sequence information for the genes.

33. A computer system of claim 31, wherein the database further comprises information identifying the expression level for the genes in normal breast tissue.

34. A computer system of claim 31, wherein the database further comprises information identifying the expression level for the genes in breast cancer tissue.

35. A computer system of claim 34, wherein the breast cancer tissue comprises infiltrating ductal carcinoma cells.

36. A computer system of claim 34, wherein the breast cancer tissue comprises microinvasive breast cancer cells.

37. A computer system of any of claims 31-36, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.

38. A computer system of claim 37, wherein the external database is GenBank.

39. A method of using a computer system of any one of claims 31-36 to present information identifying the expression level in a tissue or cell of at least one gene in Tables 1-5, comprising:

(a) comparing the expression level of at least one gene in Tables 1-5 in the tissue or cell to the level of expression of the gene in the database.

40. A method of claim 39, wherein the expression level of at least two genes are compared.

41. A method of claim 39, wherein the expression level of at least five genes are compared.

42. A method of claim 39, wherein the expression level of at least ten genes are compared.

43. A method of claim 39, further comprising displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level in breast cancer.

44. A kit comprising at least one solid support of any one of claims 24-30 packaged with gene expression information for said genes.

45. A kit of claim 44, wherein the gene expression information comprises gene expression levels in a breast cancer tissue or cell sample.

46. A kit of claim 45, wherein the gene expression information is in an electronic format.

Figure 1

Topoisomerase II alpha

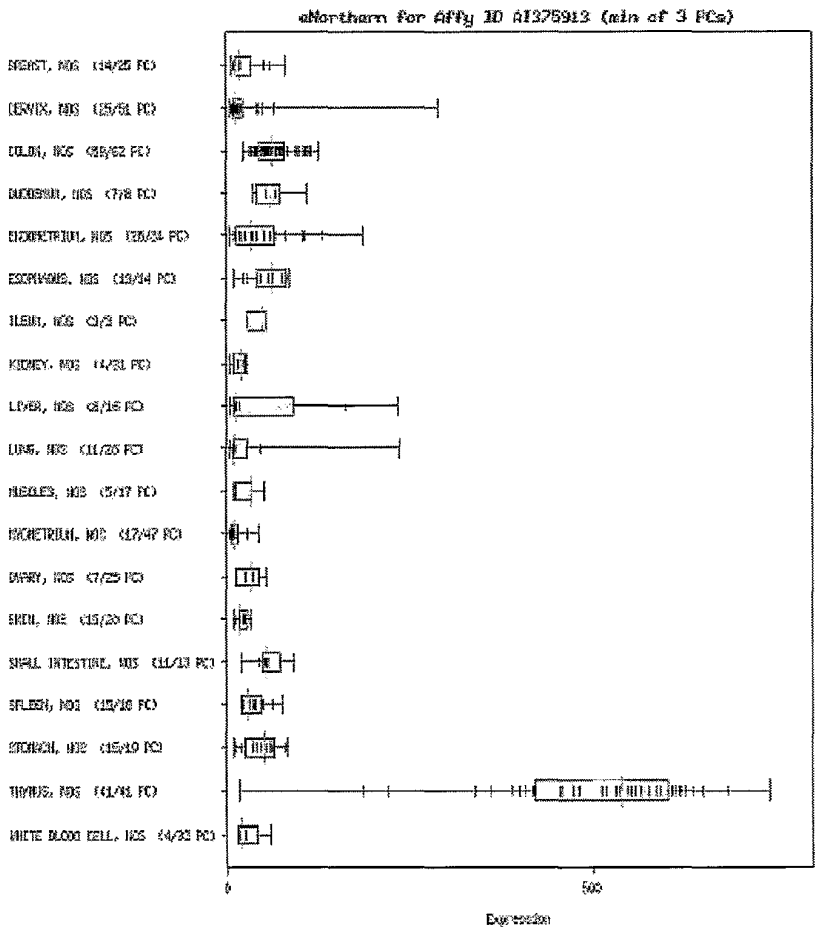
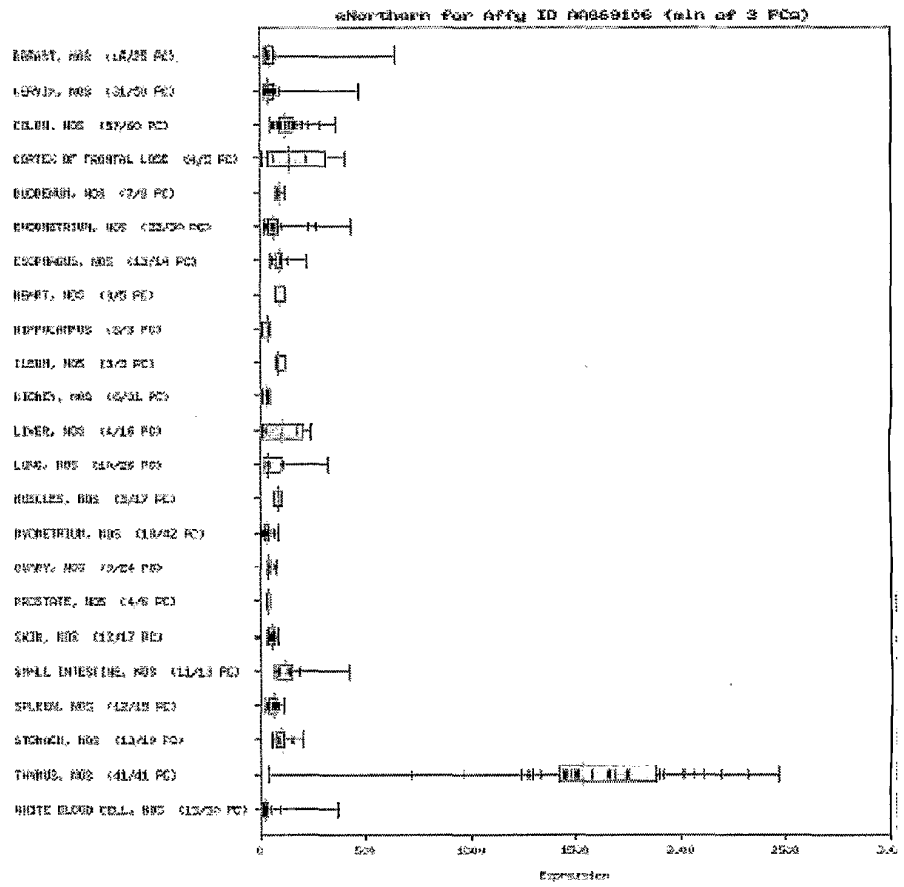


Figure 2

ICBP90



Expression

Figure 3

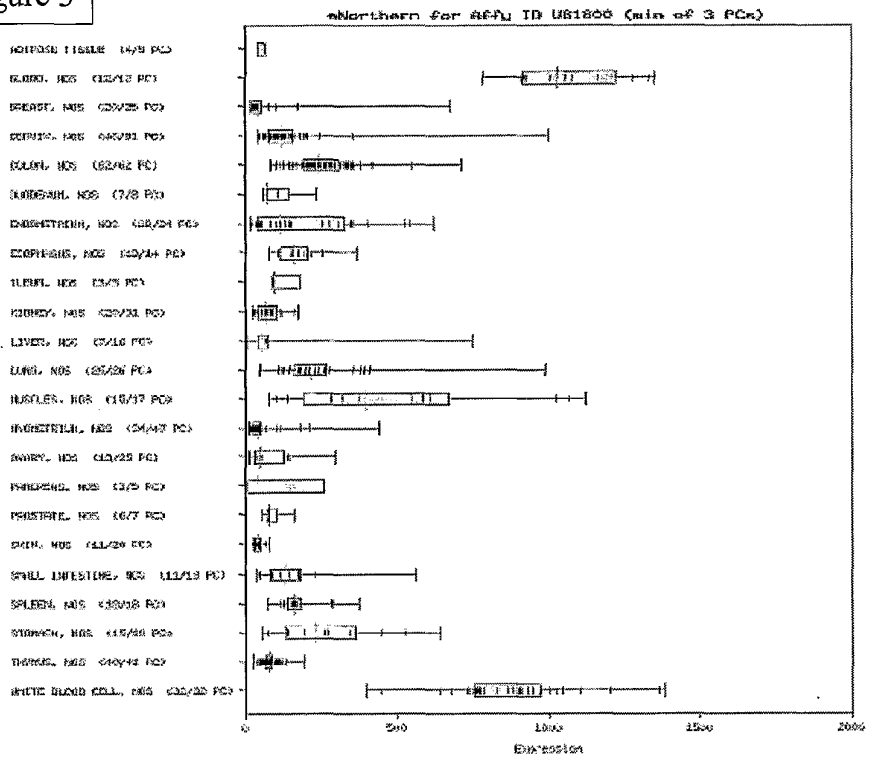


Figure 4

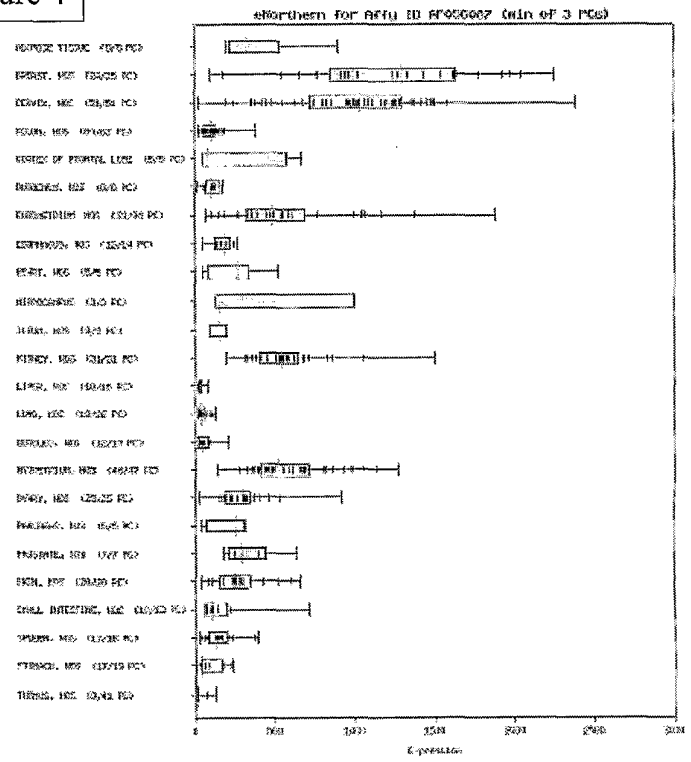


Figure 5

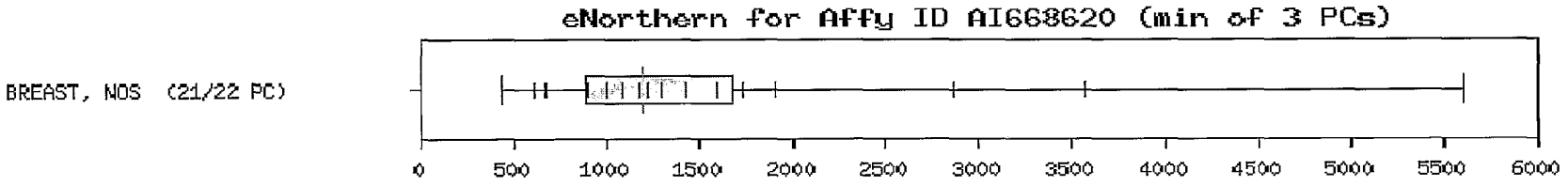
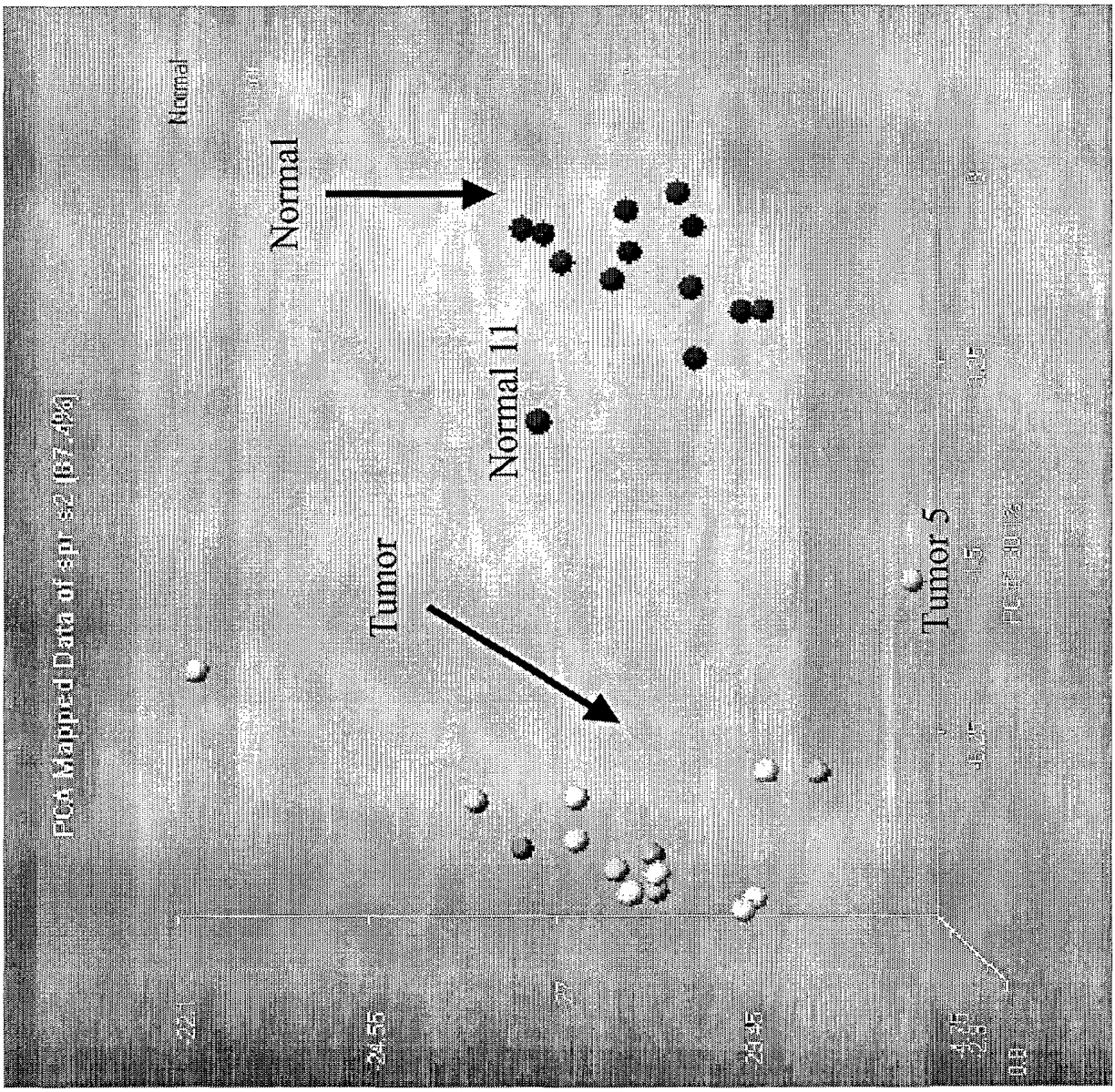
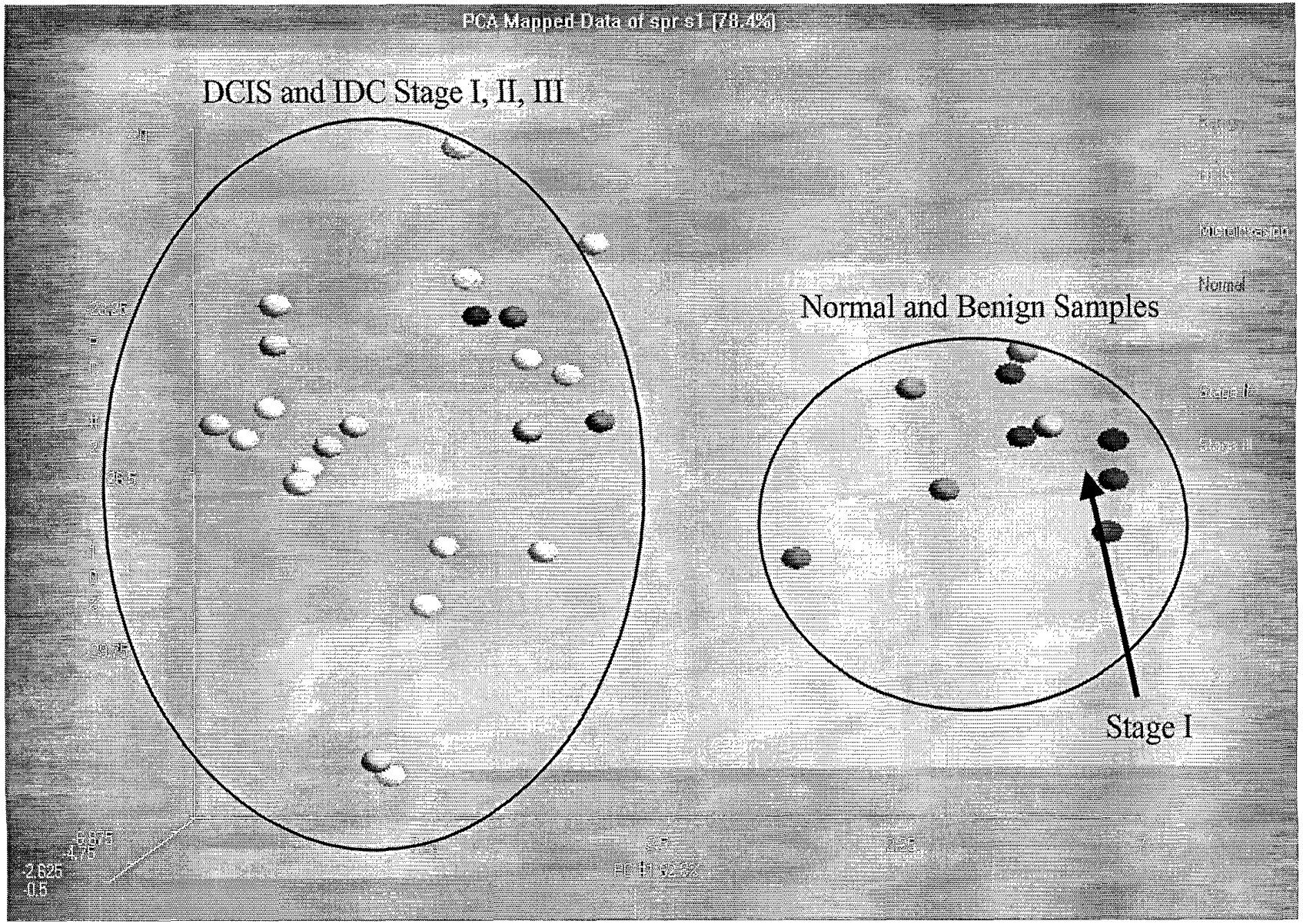


Figure 6- 28 Tissue Samples



Atty Ref 44921-5070-WO/173678

Figure 7- 33 Tissue Samples



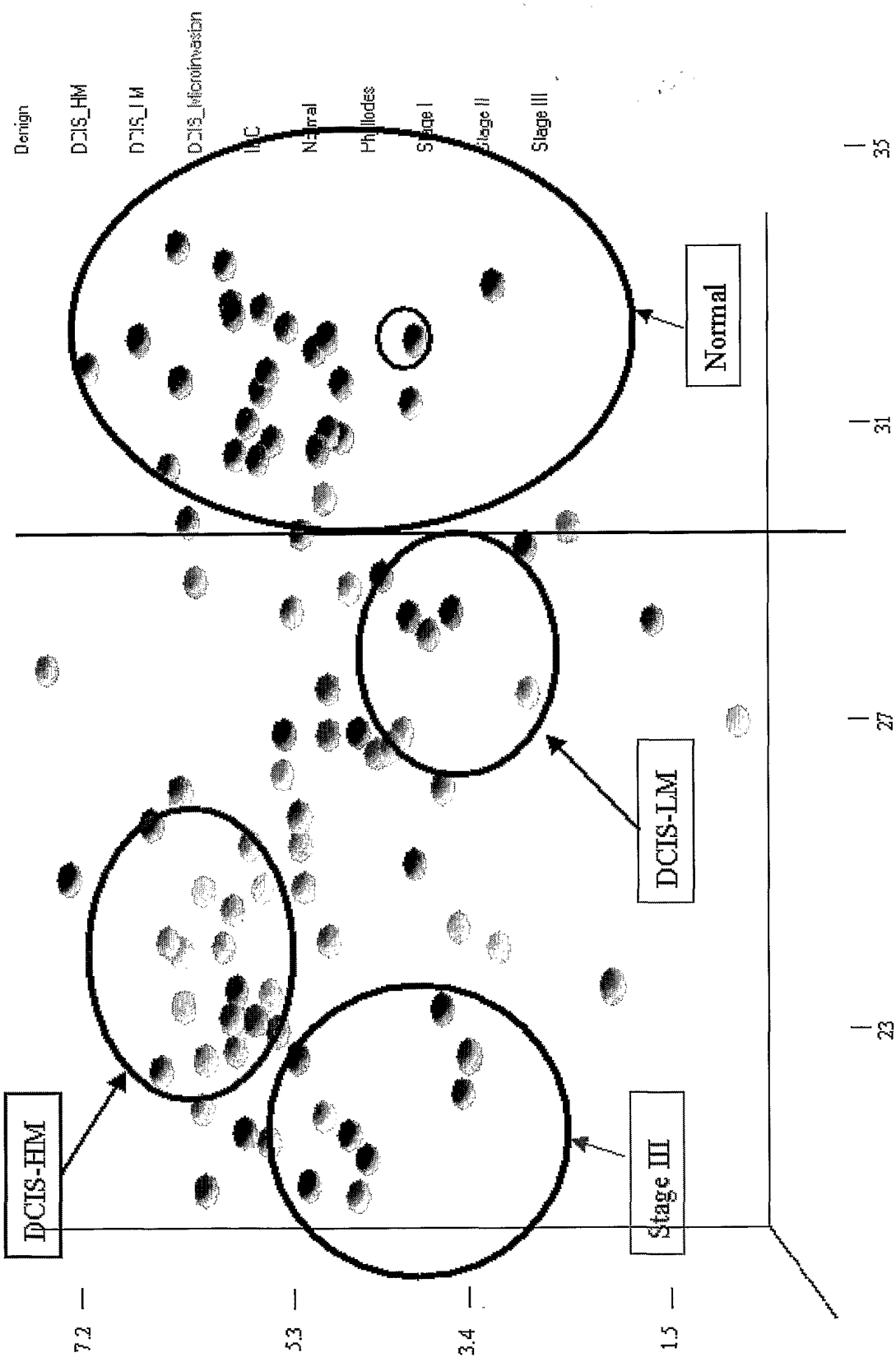


Figure 8- 91 Tissue Samples

Atty Ref 44921-5070-WO/1737678

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
1 August 2002 (01.08.2002)

PCT

(10) International Publication Number
WO 02/059271 A3

(51) International Patent Classification[7]: G01N 33/48

(21) International Application Number: PCT/US02/02176

(22) International Filing Date: 25 January 2002 (25.01.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/263,757	25 January 2001 (25.01.2001)	US
60/286,090	25 April 2001 (25.04.2001)	US
60/292,517	23 May 2001 (23.05.2001)	US

(71) Applicant *(for all designated States except US)*: **GENE LOGIC, INC.** [US/US]; 708 Quince Orchard Road, Gaithersburg, MD 20878 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **ORR, Michael, S.** [US/US]; c/o GENE LOGIC, INC., 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). **NATION, Michele** [US/US]; c/o GENE LOGIC, INC., 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). **DIGGANS, James, C.** [US/US]; c/o GENE LOGIC, INC., 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). **ZENG, Wen** [CN/US]; c/o GENE LOGIC, INC., 708 Quince Orchard Road, Gaithersburg, MD 20878 (US).

(74) Agent: **MORGAN, LEWIS & BOCKIUS LLP**; TUSCAN, Michael S., WEIMAR, Elizabeth C. et al., 1111 Pennsylvania Avenue, N.W., Washington, DC 20004 (US).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *with international search report*

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments*

— *with sequence listing part of description published separately in electronic form and available upon request from the International Bureau*

(88) Date of publication of the international search report: 7 November 2002

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 02/059271 A3

(54) Title: GENE EXPRESSION PROFILES IN BREAST TISSUE

(57) Abstract: The present invention results from the examination of tissue from breast carcinomas to identify genes differentially expressed between tumor biopsies and normal tissue. The invention includes diagnostic and screening methods using these genes as well as solid supports comprising oligonucleotide arrays that are complementary to or hybridize to the differentially expressed genes.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/02176

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : G01N 33/48

US CL : 702/19

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 702/19

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y,P	US 6,312,909 B1 (SHYJAN et al) 06 November 2001 (06.11.2001), the entire document.	1-46
Y	US 5,759,776 A (SMITH et al) 02 June 1998 (02.06.1998), the entire document.	1-46
Y	US 5,776,683 A (SMITH et al) 07 July 1998 (07.06.1998), the entire document.	1-46
A	US 6,040,138 A (LOCKHART et al) 21 March 2000 (21.03.2000), the entire document.	1-46

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"&" document member of the same patent family

Date of the actual completion of the international search

26 August 2002 (26.08.2002)

Date of mailing of the international search report

12 SEP 2002

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703)305-3230

Authorized officer

Shubo "Joe" Zhou

Telephone No. (703)-308-0196

Form PCT/ISA/210 (second sheet) (July 1998)